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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:07:51 ; Search time 77 Seconds  
(without alignments)  
992.882 Million cell updates/sec

Title: US-10-650-123-2  
Perfect score: 868  
Sequence: 1 MKKALATIALPALPAALAE.....VNTKVNRSGLSVGRVKF 174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003s:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2 AAW04891	Aaw04891 Proteinase
2	868	100.0	174	6 ABU79079	Abu79079 N. mening
3	868	100.0	174	7 ADP43316	Adp43316 N. mening
4	868	100.0	174	8 ADL16114	Adl16114 Neisseria
5	868	100.0	174	8 ADL13428	Adl13428 Neisseria
6	868	100.0	174	8 ADL24352	Adl24352 N. meningi
7	868	100.0	174	9 AEA03010	Aea03010 Neisseria
8	864	99.5	174	8 ADP08236	Adp08236 Neisseria
9	864	99.5	174	9 AEB93444	Aeb93444 Neisseria
10	857	98.7	174	8 ADL24383	Adl24383 N. meningi
11	854	98.4	174	2 AAW04893	Aaw04893 Proteinase
12	825	95.0	174	2 AAW04894	Aaw04894 Proteinase
13	825	95.0	174	5 AEG91063	Abg91063 Neisseria
14	824.5	95.0	175	2 AAW04892	Aaw04892 Proteinase
15	820	94.5	166	8 ADL24385	Adl24385 N. meningi
16	809.5	93.3	175	6 AEB77991	Abp77991 N. gonorr
17	794	91.5	162	8 ADL24387	Adl24387 N. meningi
18	793	91.4	162	8 ADL24386	Adl24386 N. meningi
19	785	90.4	155	4 AAB19895	Aab19895 Neisseria
20	781	90.0	155	8 ADL13426	Adl13426 Neisseria
21	779.5	89.8	161	8 ADL24384	Adl24384 N. meningi
22	746	85.9	154	8 ADL24388	Adl24388 N. meningi
23	657.5	75.7	141	8 ADL24389	Adl24389 N. meningi
24	234	27.0	208	5 AAO17579	Aao17579 M catarrh

25	224	25.8	232	6	ABP79561	Abp79561 N. gonorr
26	221.5	25.5	176	5	AAU97605	Aau97605 Haemophil
27	221.5	25.5	176	5	AAU97603	Aau97603 Haemophil
28	221.5	25.5	176	5	AAU97602	Aau97602 Haemophil
29	221.5	25.5	176	5	AAU97604	Aau97604 Haemophil
30	218.5	25.2	229	6	ABP79854	Abp79854 N. gonorr
31	218	25.1	226	6	ABP79754	Abp79754 N. gonorr
32	214.5	24.7	176	5	AAU97601	Aau97601 Haemophil
33	214	24.7	281	6	ABP80738	Abp80738 N. gonorr
34	212	24.4	278	6	ABP80098	Abp80098 N. gonorr
35	210	24.2	265	6	ABP77624	Abp77624 N. gonorr
36	208	24.0	161	9	ABE91376	Aeb91376 Microbial
37	207.5	23.9	186	6	ABP80662	Abp80662 N. gonorr
38	206	23.7	241	9	ABE93440	Aeb93440 Neisseria
39	206	23.7	278	6	ABP80428	Abp80428 N. gonorr
40	204.5	23.6	229	6	ABP77612	Abp77612 N. gonorr
41	194.5	22.4	227	6	ABP77150	Abp77150 N. gonorr
42	194.5	22.4	227	6	ABP76762	Abp76762 N. gonorr
43	178	20.5	189	6	ABP78327	Abp78327 N. gonorr
44	141	16.2	27	8	ADL27222	Adl27222 Peptide f
45	141	16.2	27	9	ABE87498	Aeb87498 Neisseria

## ALIGNMENTS

RESULT 1  
AAW04891  
ID AAW04891 standard; protein; 174 AA.  
AC AAW04891;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-DEC-1996 (first entry)  
DE Proteinase K resistant N. meningitidis 22 kD surface protein.  
XX  
KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
KW antibody; detection; probe; surface protein.  
XX  
OS Neisseria meningitidis; strain 608B.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= sig\_peptide  
FT Protein 20..174  
FT /label= mat\_protein  
XX  
PN W03620442-AL  
PD 26-SEP-1996.  
XX  
PF 15-MAR-1996; 96MO-CA000157.  
XX  
PR 17-MAR-1995; 95US-00406362.  
PR 04-AUG-1995; 95US-0001983P.  
XX  
PA (IAFPB-) IAF BIO VAC INC.  
XX  
PI Brodeur BR, Martin D, Hamel J, Rioux C;  
XX  
WI 1996-443187/44.  
XX  
DR N-PSDB; AAT39039.  
XX  
PS Neisseria meningitidis antigen, highly conserved between different  
PT strains - useful for proddn. of antibodies for immunisation against, or  
diagnosis of, N. meningitidis infection.  
XX  
PS Claim 7; Fig 1; 117pp; English.  
XX  
CC A proteinase K resistant surface protein has been isolated from 4 strains  
CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,  
CC antigenic fragments of antibodies can be used in a vaccine for the

1-6885-98

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CC prevention of infection by N. meningitidis or by N. gonorrhoeae in  
 CC humans. The antibodies may also be used diagnostically to detect N.  
 CC meningitidis infection. The antigen may also be used to detect antibodies  
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,  
 CC or their fragments, can be used as probes for the detection of pathogenic  
 CC *Neisseria* bacteria. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 174 AA;

Query Match 100.0%; Score 868; DB 2; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;  
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 QY 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNRSGELSGVGRVKF 174  
 DB 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNRSGELSGVGRVKF 174

RESULT 2  
 ABU79079  
 ID ABU79079 standard; protein; 174 AA.  
 XX  
 AC ABU79079;  
 DT 18-JUN-2003 (first entry)  
 XX  
 DE N. meningitidis lipopolysaccharide protein.  
 XX  
 KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;  
 KW gene therapy; mammalian cell receptor; cytostatic;  
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;  
 KW tumouricidal immunocyte; antitumour.  
 XX  
 OS *Neisseria meningitidis*.



XX US2002177551-A1.  
 XX 28-NOV-2002.  
 XX 30-MAY-2001; 2001US-00870759.  
 XX 31-MAY-2000; 2000US-0208128P.  
 XX (TERM/) Terman D S.  
 XX Terman DS;  
 XX  
 XX WPI; 2003-361759/34.  
 XX N-PSDB; ACA64711.  
 XX  
 XX A mammalian cell receptor, useful in the treatment of cancer by binding  
 XX to tumor associated lipids where the binding induces anergy or apoptosis  
 XX in T cells and antigen presenting cells.  
 XX  
 XX Disclosure; Page; 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the  
 XX treatment of cancer, which binds to tumour associated lipids and induces  
 XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).  
 XX Also included are a mammalian cell useful in the treatment of cancer  
 XX where the receptor which binds tumour associated lipids and induces  
 XX cellular inactivation or death is deleted or functionally deactivated.  
 XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal  
 XX (by allowing tumour associated lipids to contact immunocytes in which  
 XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,

CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,  
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or  
 CC deleted), a construct useful in the treatment of cancer comprising a  
 CC superantigen (Sag) nucleotide inserted into a virus, a mammalian T cell  
 CC useful in the treatment of cancer (where an adaptor protein which  
 CC inhibits T cell activation by tumour associated antigens is deleted or  
 CC functionally deactivated), a composition useful in the treatment of  
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing  
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by  
 CC allowing tumour associated lipids to contact immunocytes, in which  
 CC receptors for the lipids are inactivated or deleted to produce a  
 CC tumouricidal immunocyte population, and administering the tumouricidal  
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC  
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to  
 CC contact APCs, in which receptors for the tumour associated lipids are  
 CC inactivated or deleted to produce a tumouricidally activated population,  
 CC and administering APCs to the host), producing a tumouricidal T cell  
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to  
 CC contact T cells, in which adaptor proteins, which inhibit T cell  
 CC activation by tumour associated antigens, are deleted or functionally  
 CC deactivated to produce a tumouricidal population of T cells, and  
 CC administering the tumouricidally activated T cells to the host, or  
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and  
 CC administering the tumouricidally activated T cells to the host), treating  
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which  
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)  
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a  
 CC tumour associated antigen to contact immunocytes in which adaptor  
 CC proteins which inhibit T cell activation by tumour associated antigens  
 CC are deleted or functionally deactivated) and producing (M7) a  
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a  
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The  
 CC receptors, methods and compositions are useful for treating cancers and  
 CC tumours. Bacterial superantigens are co-administered or administered as  
 CC fusion constructs with anti-tumour proteins or motifs. The present  
 CC sequence represents an anti-tumour protein which is co-administered with  
 CC or incorporated into a fusion construct with a superantigen. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from the US patent  
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"  
 XX  
 SQ Sequence 174 AA;

Query Match 100.0%; Score 868; DB 6; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;  
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 QY 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNRSGELSGVGRVKF 174  
 DB 121 SQTSGIGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNRSGELSGVGRVKF 174  
 RESULT 3  
 ADF43316  
 ID ADF43316 standard; protein; 174 AA.  
 XX  
 AC ADF43316;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE N. meningitidis lipopolysaccharide seq id 36.  
 XX  
 KW receptor; lipid-based tumour associated antigen; cytostatic;  
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;  
 KW infectious disease; lipopolysaccharide; LPS.

XX OS Neisseria meningitidis.  
XX PN US2003157113-A1.  
XX PD 21-AUG-2003.  
XX PF 28-DEC-2000; 2000US-00751708.  
XX PR 28-DEC-1999; 99US-0173371P.  
XX PA (TERM/) Terman D S.  
XX PI Terman DS;  
XX DR WPI; 2003-787326/74.  
XX DR N-PSDB; ADP43315.  
XX XX  
XX XX New receptor in a mammalian cell that inhibits regular activation by  
XX PT receptors specific for lipid-based tumor associated antigens, useful for  
XX PT treating a neoplastic disease or tumor, and infectious diseases.  
XX PS Disclosure; SEQ ID NO 36; 151pp; English.  
XX XX  
XX CC The invention describes a receptor in a mammalian cell that inhibits  
XX CC regular activation by receptors specific for lipid-based tumor  
XX CC associated antigen. The receptor has cytostatic and antimicrobial  
XX CC properties and is suitable for use in gene therapy. The receptors,  
XX CC methods and compositions are useful for treating a neoplastic disease or  
XX CC tumor (cancer), and infectious diseases. This is the amino acid sequence  
XX CC of Neisseria meningitidis lipopolysaccharide (LPS) to which tumour cells  
XX CC develop immunity.  
XX SQ Sequence 174 AA;  
  
Query Match 100.0%; Score 868; DB 7; Length 174;  
Best Local Similarity 100.0%; Pred. No. 1.1e-86;  
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
  
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGSDSF 120  
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGSDSF 120  
  
QY 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174  
DB 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174  
  
RESULT 4  
ADL16114  
ID ADL16114 standard; protein; 174 AA.  
AC ADL16114;  
XX XX  
XX XX 03-JUN-2004 (first entry)  
XX DE Neisseria meningitidis NspA for use in vaccine.  
XX KW Outer membrane vesicle preparation; OMV; detergent-free;  
XX KW physical disruption; vaccine; serogroup B; NspA;  
XX KW Neisserial surface protein A; immunogen.  
XX OS Neisseria meningitidis.  
XX PN WO2004019977-A2.  
XX PD 11-MAR-2004.  
XX PF 01-SEP-2003; 2003WO-IB004293.

XX PR 30-AUG-2002; 2002GB-00020194.  
XX PA (CHIR ) CHIRON SRL.  
XX PI Pizza M, Serruto D, Rappuoli R;  
XX DR WPI; 2004-239124/22.  
XX XX  
XX PT Producing an outer membrane vesicle (OMV) preparation from a bacterium,  
XX PT useful as a vaccine against Neisseria meningitidis serogroup B, comprises  
XX PT disrupting the bacterial membrane in the absence of deoxycholate  
XX PT detergent.  
XX PS Disclosure; Fig 3; 20pp; English.  
XX XX  
XX CC The invention relates to a process for producing an outer membrane  
XX CC vesicle (OMV) preparation from a bacterium. The process involves  
XX CC disrupting the bacterial membrane substantially in the absence of  
XX CC deoxycholate detergent or other detergent, followed by several  
XX CC centrifugation steps. Membrane disruption is achieved by sonication,  
XX CC homogenisation, microfluidisation, cavitation, osmotic shock, grinding,  
XX CC French press, belnding or any other physical technique. The outer  
XX CC membrane vesicles can be prepared from bacteria of the genera Moraxella,  
XX CC Shigella, Pseudomonas, Treponema, Porphyromonas, Helicobacter or  
XX CC Neisseria, and are particularly produced from Neisseria meningitidis  
XX CC (especially serogroup B) or Neisseria gonorrhoeae. The invention also  
XX CC relates to a Neisseria meningitidis outer membrane vesicle composition in  
XX CC which the vesicles include the immunogens NspA (Neisserial surface  
XX CC protein A; ADL16114), 287 protein (ADL16113) and 741 protein (ADL16112);  
XX CC and the use of outer membrane vesicle compositions as a medicament,  
XX CC especially for raising an immune response in a patient. The method is  
XX CC useful for manufacturing an outer membrane vesicle preparation as a  
XX CC vaccine against Neisseria meningitidis serogroup B. The present sequence  
XX CC represents Neisseria meningitidis NspA.  
XX SQ Sequence 174 AA;  
  
Query Match 100.0%; Score 868; DB 8; Length 174;  
Best Local Similarity 100.0%; Pred. No. 1.1e-86;  
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
  
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGSDSF 120  
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGSDSF 120  
  
QY 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174  
DB 121 SQTSLGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174  
  
RESULT 5  
ADL13428  
ID ADL13428 standard; protein; 174 AA.  
XX XX  
XX AC ADL13428;  
XX XX  
XX DT 03-JUN-2004 (first entry)  
XX XX  
XX DE Neisseria meningitidis H44/76 full-length NspA protein.  
XX KW Neisserial surface protein A; NspA; refolding; recombinant production;  
XX KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;  
XX KW invasive bacterial disease; bacteraemia; meningitis;  
XX KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;  
XX KW antibacterial; gene therapy.  
XX XX  
XX OS Neisseria meningitidis; H44/76.  
XX XX

FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT Protein 20..174  
 FT Misc-difference 168  
 FT /note= "The corresponding residue in the mature protein shown in Fig 2 (residue 149) is Ala"  
 XX WO2004020452-A2.  
 XX 11-MAR-2004.  
 XX 28-AUG-2003; 2003WO-EP010085.  
 XX 30-AUG-2002; 2002GB-00020197.  
 XX (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.  
 XX (UYUT-) RIJKSUNIV UTRECHT.  
 XX Biemans R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;  
 XX Tommassen J, Weynants V;  
 XX WPI; 2004-239150/22.  
 XX N-PSDB; ADL13427.  
 XX New refolded NspA protein, useful for preparing a composition for  
 XX diagnosing, treating or preventing infection caused by *Neisseria*  
 XX meningitidis or *Neisseria gonorrhoeae*.  
 XX Disclosure; Fig 3; 62pp; English.  
 XX The invention relates to an isolated refolded *Neisseria* surface protein  
 XX A (NspA) from *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The  
 XX invention also relates to the method of refolding an NspA protein; an  
 XX alkaline refolding buffer comprising ethanolamine and SB-12 (3-  
 XX dimethyldecylammonopropanesulphonate) for refolding an NspA protein; a  
 XX pharmaceutical composition comprising the refolded NspA protein, a  
 XX carrier and optionally one or more other *Neisseria* antigens; a method of  
 XX preventing or treating a *Neisseria* infection; an antibody immunospecific  
 XX for the NspA protein; and diagnosing a *Neisseria* infection. NspA has  
 XX characteristics which indicate that it is a potential vaccine candidate  
 XX for the development of subunit vaccines for the treatment of infections  
 XX caused by *Neisseria meningitidis* (meningococcus), which causes invasive  
 XX bacterial diseases such as bacteraemia and meningitis, or *Neisseria*  
 XX gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced  
 XX NspA could therefore be used to produce vaccine compositions and it could  
 XX also be used in the development of new antimicrobial agents, diagnostic  
 XX tests and in drug screening. However, recombinantly produced proteins are  
 XX frequently unable to adopt their biologically active conformations, and  
 XX yields may be very low due to mis-folding and aggregation of the protein.  
 XX The method of the invention provides an improved method for refolding the  
 XX NspA protein, and it is possible to increase the recovery of active  
 XX protein form partly purified inclusion bodies in amounts up to 100%  
 XX without the need for further purification. The refolded NspA protein is  
 XX useful for preparing a composition for diagnosing, treating or preventing  
 XX infection caused by *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The  
 XX present sequence represents the full-length NspA protein from *Neisseria*  
 XX meningitidis H44/76.  
 XX Sequence 174 AA;  
 XX Query Match 100.0%; Score 868; DB 8; Length 174;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-86;  
 XX Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120  
 Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRYNYIGKVTNTKQVRSGLSVGVVRVKF 174  
 Db 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRYNYIGKVTNTKQVRSGLSVGVVRVKF 174  
 RESULT 6  
 ADL24352  
 ID ADL24352 standard; protein; 174 AA.  
 XX AC ADL24352;  
 XX 03-JUN-2004 (first entry)  
 XX N meningitidis strain 608B NspA protein.  
 XX NspA; vaccine; antibacterial; meningitis.  
 XX *Neisseria meningitidis*.  
 XX WO2004019976-A2.  
 XX 11-MAR-2004.  
 XX 29-AUG-2003; 2003WO-CA001452.  
 XX 30-AUG-2002; 2002US-0406980P.  
 XX (SHIR-) SHIRE BIOCHEM INC.  
 XX Martin D, Rioux S;  
 XX WPI; 2004-239123/22.  
 XX N-PSDB; ADL24351.  
 XX Composition comprising liposome associated with isolated polypeptide or  
 XX polynucleotide derived from *Neisseria meningitidis* strain 608B, or its  
 XX fragment or analog, useful for inducing an immune response against N.  
 XX meningitidis.  
 XX Claim 1; Fig 1; 79pp; English.  
 XX The present invention relates to a pharmaceutical composition comprising  
 XX a liposome associated with an isolated polypeptide derived from *Neisseria*  
 XX meningitidis strain 608B, where the polypeptide is the NspA protein. The  
 XX composition is useful for inducing an immune response against N.  
 XX meningitidis, for preventing and/or treating N. meningitidis infection  
 XX and for treating and/or preventing *Neisseria* infection chosen from N.  
 XX meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is  
 XX useful for treatment or prophylaxis of meningitis and meningococcaemia, in  
 XX a host. The host is a mammal, preferably a human and more preferably an  
 XX adult human. The present sequence is the *Neisseria meningitidis* strain  
 XX 608B NspA protein.  
 XX Sequence 174 AA;  
 XX Query Match 100.0%; Score 868; DB 8; Length 174;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-86;  
 XX Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120  
 Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120  
 QY 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRYNYIGKVTNTKQVRSGLSVGVVRVKF 174  
 Db 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRYNYIGKVTNTKQVRSGLSVGVVRVKF 174



RESULT 7

AEAO3010  
ID AEAO3010 standard; protein; 174 AA.

XX AC AEAO3010;

XX DT 28-JUL-2005 (first entry)

XX DE Neisseria meningitidis meningococcal meningitis protein SEQ ID NO:36.

XX KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic; meningitis.

XX OS Neisseria meningitidis.

XX PN US2005112141-A1.

XX PD 26-MAY-2005.

XX PF 08-SEP-2004; 2004US-00937758.

XX PR 30-AUG-2000; 2000US-00650884.

XX PA (TERM/) Terman D S.

XX PI Terman DS;

XX DR WPI; 2005-394926/40.

XX DR N-PSDB; AEAO3009.

XX PT New composition for treating a tumor or neoplastic disease in a subject  
comprises conjugates comprising superantigen polypeptides or nucleic  
acids with other molecules that produce a tumoricidal response.

XX PS Disclosure; SEQ ID NO 36; 125pp; English.

XX CC The invention relates to a composition for treating a tumor or neoplastic  
disease in a subject. Also described: (1) a mammalian cell comprising an  
exogenous nucleic acid encoding a superantigen expressed in the cell,  
which cell also produces or expresses all alpha-anomers of  
monoglycosylceramide or diglycosylceramide, where expression of the  
superantigen and the mono- or diglycosylceramide is capable of eliciting  
an antitumor immune response in a mammal into which the cell is  
introduced; (2) treating a tumor or neoplastic disease in a subject; (3)  
preparing a population of immunotherapeutic T or natural killer T (NKT)  
cells useful to treat a tumor or neoplastic disease in a subject; (4) an  
apoptotic cell preparation or lysate useful for treating a tumor or  
neoplastic disease in a subject, comprising a cell population that has  
been transfected with naked DNA encoding a superantigen, and treated to  
undergo apoptosis or lysis; and (5) a cell that has ingested or been  
transfected with the above apoptotic preparation or lysate, thus,  
rendering the cell effective in presenting material expressed from  
transfecting nucleic acid or material ingested to the immune system of a  
mammal to elicit an anti-tumor immune response. The composition and  
methods are useful for treating tumors or neoplastic diseases. The  
present sequence represents a Neisseria meningitidis protein sequence  
which induces meningococcal meningitis, which is given in the  
exemplification of the present invention. Note - The sequence data for  
this patent is not represented in the printed specification, but was  
obtained in electronic format directly from the USPTO web site.

XX SQ Sequence 174 AA;

Query Match 100.0%; Score 868; DB 9; Length 174;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTNKNVRSGLSVGVRYKF 174  
DB 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTNKNVRSGLSVGVRYKF 174

RESULT 8

ADP08236

XX AC ADP08236 standard; protein; 174 AA.

XX AC ADP08236;

XX DT 26-AUG-2004 (first entry)

XX DE Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 69.

XX KW outer-membrane vesicle; antibacterial; antiinflammatory;  
meningococcal protein trafficking; localisation; infection; vaccine;  
gene therapy.

XX OS Neisseria meningitidis MC58.

XX PN W02004046427-A2.

XX PD 03-JUN-2004.

XX PF 17-NOV-2003; 2003WO-IB006281.

XX PR 15-NOV-2002; 2002GB-00026734.

XX PR 27-MAR-2003; 2003GB-00007131.

XX PA (CHIR ) CHIRON SRL.

XX PI Norais N, Grandi G;

XX DR WPI; 2004-420615/39.

XX CC New compositions having outer-membrane vesicles and proteins from  
Neisseria meningitidis, useful in the field of meningococcal  
biochemistry, in particular for preventing and/or treating meningococcal  
infections.

XX PS Claim 9; SEQ ID NO 69; 79pp; English.

XX CC The invention relates to a novel composition comprising outer-membrane  
vesicles (OMV) prepared from a first strain of Neisseria meningitidis and  
1 or more proteins which are present in OMVs prepared from a second  
strain of N. meningitidis, but which are not present in OMVs prepared  
from the first strain. The composition of the invention demonstrates  
antibacterial and antiinflammatory activities and may be useful in the  
field of meningococcal biochemistry, in particular the trafficking and  
localisation of meningococcal proteins, as well as in the prevention or  
treatment of meningococcal infections, possibly via the production of a  
vaccine or gene therapy. The current sequence is that of a Neisseria  
meningitidis MC58 outer-membrane vesicle (OMV)-related membrane protein  
of the invention.

XX SQ Sequence 174 AA;

Query Match 99.5%; Score 864; DB 8; Length 174;

Best Local Similarity 99.4%; Pred. No. 2.9e-86;

Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTNKNVRSGLSVGVRYKF 174

DB 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRYNYIGKVTNKNVRSGLSVGVRYKF 174

121 SQTSGIGLVLTGVSVAVTNPVNDLDAGYRNYIGKVTNTKVRSGELSGVRVKF 174

Db

RESULT 9  
AEB93444 standard; protein; 174 AA.

AC AEB93444;

XX 20-OCT-2005 (first entry)

XX Neisseria meningitidis group B surface protein A.  
XX protein quantitation; surface protein A.

XX Neisseria meningitidis serogroup B.

XX US2005176085-A1.

XX 11-AUG-2005.

XX 15-NOV-2004; 2004US-00988943.

XX 19-NOV-2003; 2003CU-00000269.

XX (BETA/) BETANCOURT N L H.  
XX (DORT/) DORTA-DUQUE J F D C.  
XX (PERE/) PEREZ V A B.  
XX (VALD/) VALDES J G.  
XX (LOPE/) LOPEZ L J G.  
XX (PALO/) PALOMARES G R P.  
XX (FEYT/) FEYT R P.  
XX (GILF/) GIL F M A.

XX Betancourt NLH, Dorta-Duque JFD, Perez VAB, Valdes JG, Lopez LJG;  
XX Palomares GRP, Feyt RP, Gil FMA;  
XX WPI; 2005-596348/61.

XX Identifying and quantifying proteins in complex mixtures by selectively  
XX isolating peptides not containing histidine nor arginine from each  
XX protein, and determining the relative concentration of proteins in  
XX different samples.

XX Example 2; SEQ ID NO 20; 91pp; English.

XX The invention relates to a method for identifying and quantifying one or  
XX more proteins in complex mixtures by selectively isolating peptides not  
XX containing histidine nor arginine (NHR peptides) from each protein, and  
XX determining the relative concentration of one or more proteins in  
XX different samples from the ratio between the areas of estimated  
XX theoretical spectra for each NHR peptide labeled with different isotopes  
XX in each sample. The method comprises: (a) enzymatically or chemically  
XX hydrolyzing the sample or samples of proteins; (b) chemically modifying  
XX alpha and epsilon amino groups (alpha- and epsilon-NH2) of every peptide  
XX obtained in step (a); (c) isolating the NHR peptides by cation exchange  
XX chromatography from the mixture of peptides obtained in step (b); (d)  
XX identifying proteins by mass spectrometry analysis of the NHR peptides  
XX obtained in step (c); (e) differential isotopic labeling of protein  
XX samples previously to step (a) or during steps (a) or (b) and immediately  
XX mixing at least a portion of the samples; and (f) relative quantifying of  
XX more proteins in the mixtures of step (e) from the ratio between the  
XX areas of estimated theoretical spectra of the pair of NHR peptides  
XX identified in step (d), as well as from the ratio between the areas of  
XX the estimated theoretical spectra of fragments from the NHR peptides,  
XX generated in step (d). Also described is a kit for the identification and  
XX quantification of proteins in complex mixtures, which comprises the  
XX method mentioned above. The method and kit are useful for identifying or  
XX quantifying proteins, such as those with vaccinal, therapeutic or  
XX diagnostic uses, in complex mixtures. The present sequence represents a  
XX surface protein A, which is used in an example from the present  
XX invention.

SQ Sequence 174 AA;

Query Match 99.5%; Score 864; DB 9; Length 174;  
Best Local Similarity 99.4%; Pred. No. 2.9e-86;  
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKXKAPSTDFKLYSGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

Db 61 FAVDYTRYKXKAPSTDFKLYSGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTNPVNDLDAGYRNYIGKVTNTKVRSGELSGVRVKF 174

Db 121 SQTSGIGLVLTGVSVAVTNPVNDLDAGYRNYIGKVTNTKVRSGELSGVRVKF 174

RESULT 10

ID ADL24383 standard; protein; 174 AA.

XX ADL24383;

XX 03-JUN-2004 (first entry)

XX N meningitidis strain 608B modified NspA protein #1.

XX mutein; mutant; NspA; vaccine; antibacterial; meningitis.

XX Neisseria meningitidis.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 115 /note= "wild-type Gly substituted by Ala"

XX Misc-difference 118 /note= "wild-type Asp substituted by Asn"

XX WO2004019976-A2.

XX 11-MAR-2004.

XX 29-AUG-2003; 2003WO-CA001452.

XX 30-AUG-2002; 2002US-0406980P.

XX (SHIR-) SHIRE BIOCHEM INC.

XX Martin D, Rioux S;

XX WPI; 2004-239123/22.

XX Composition comprising liposome associated with isolated polypeptide or  
XX polynucleotide derived from Neisseria meningitidis strain 608B, or its  
XX fragment or analog, useful for inducing an immune response against N.  
XX meningitidis.

XX Example 4; Page; 79pp; English.

XX The present invention relates to a pharmaceutical composition comprising  
XX a liposome associated with an isolated polypeptide derived from Neisseria  
XX meningitidis strain 608B, where the polypeptide is the NspA protein. The  
XX composition is useful for inducing an immune response against N.  
XX meningitidis, for preventing and/or treating N. meningitidis infection  
XX and for treating and/or preventing neisserial infection chosen from N.  
XX meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharae. It is  
XX useful for treatment or prophylaxis of meningitis and meningococemia, in  
XX a host. The host is a mammal, preferably a human and more preferably an  
XX adult human. The present sequence is a modified version of the Neisseria  
XX meningitidis strain 608B NspA protein. Note: This sequence is not shown  
XX in the specification but has been created based on the information given

CC and the wild-type NspA protein shown in Figure 1.

XX SQ Sequence 174 AA;  
 Query Match 98.7%; Score 857; DB 8; Length 174;  
 Best Local Similarity 98.9%; Pred. No. 1.7e-85;  
 Matches 172; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSP 120  
 DB 61 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSP 120  
 QY 121 SQTSGIGLVLTGVSVAVTNNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174  
 DB 121 SQTSGIGLVLTGVSVAVTNNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174

RESULT 11  
 AAW04893  
 ID AAW04893 standard; protein; 174 AA.  
 XX AC AAW04893;  
 XX AC  
 DT 16-OCT-2003 (revised)  
 DT 22-DEC-1996 (first entry)  
 XX  
 XX Proteinase K resistant N. meningitidis 22 kd surface protein.  
 XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
 KW antibody; detection; probe; surface protein.  
 XX  
 XX Neisseria meningitidis; strain Z4063.  
 XX

Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= sig\_peptide  
 FT Protein 20..174  
 FT /label= mat\_protein  
 XX WO9629412-A1.  
 XX  
 XX 26-SEP-1996.  
 XX  
 XX 15-MAR-1996; 96WO-CA000157.  
 XX  
 XX 17-MAR-1995; 95US-00406362.  
 PR 04-AUG-1995; 95US-0001983P.  
 XX  
 XX (IAPB-) IAP BIO VAC INC.  
 PA  
 XX Brodeur BR, Martin D, Hamel J, Rioux C;  
 XX  
 XX WPI; 1996-443187/44.  
 DR N-PSDB; AAT39041.  
 XX

Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection.  
 Claim 7; Fig 9; 117pp; English.

A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kd antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic

CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)  
 XX SQ Sequence 174 AA;  
 Query Match 98.4%; Score 854; DB 2; Length 174;  
 Best Local Similarity 98.3%; Pred. No. 3.7e-85;  
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSP 120  
 DB 61 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSP 120  
 QY 121 SQTSGIGLVLTGVSVAVTNNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174  
 DB 121 SQTSGIGLVLTGVSVAVTNNVDLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174

RESULT 12  
 AAW04894  
 ID AAW04894 standard; protein; 174 AA.  
 XX AC AAW04894;  
 XX AC  
 DT 16-OCT-2003 (revised)  
 DT 22-DEC-1996 (first entry)  
 XX  
 XX Proteinase K resistant N. meningitidis 22 kd surface protein.  
 XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
 KW antibody; detection; probe; surface protein.  
 XX  
 XX Neisseria meningitidis; strain b2.  
 XX

Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= sig\_peptide  
 FT Protein 20..174  
 FT /label= mat\_protein  
 XX WO9629412-A1.  
 XX  
 XX 26-SEP-1996.  
 XX  
 XX 15-MAR-1996; 96WO-CA000157.  
 XX  
 XX 17-MAR-1995; 95US-00406362.  
 PR 04-AUG-1995; 95US-0001983P.  
 XX  
 XX (IAPB-) IAP BIO VAC INC.  
 PA  
 XX Brodeur BR, Martin D, Hamel J, Rioux C;  
 XX  
 XX WPI; 1996-443187/44.  
 DR N-PSDB; AAT39042.  
 XX

Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection.  
 Claim 7; Fig 10; 117pp; English.

A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kd antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic

```
CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 174 AA;

Query Match 95.0%; Score 825; DB 2; Length 174;
Best Local Similarity 94.3%; Pred. No. 5.6e-82;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKYNKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 120
Db 61 FAVDYTRYKYNKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRRASHLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYVTPNVVDLDAGYRNYNIGKNTVTKNVRSGELSVGVVRVKF 174
Db 121 SKTSAGLGLVLAGVSAYVTPNVVDLDAGYRNYNIGKNTVTKNVRSGELSVGVVRVKF 174

RESULT 13
ABG91063
ID ABG91063 standard; protein; 174 AA.
XX
AC ABG91063;
XX
DT 29-NOV-2002 (first entry)
XX
DE Neisseria gonorrhoeae outer membrane protein #1.
XX
KW Gram-negative bacterial bleb; PorB; outer membrane protein;
KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
KW protective antigen; antibacterial; vaccine.
XX
OS Neisseria gonorrhoeae.
XX
PN WO200262380-A2.
XX
PD 15-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-EP001356.
XX
PR 08-FEB-2001; 2001GB-00003169.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;
XX
WPI; 2002-657510/70.
XX
N-PSDB; ABS67381.
XX
Novel gram-negative bacterial bleb presenting on its surface PorB outer
membrane protein from Chlamydia trachomatis or protective antigen from
Chlamydia pneumoniae, useful for preventing Chlamydia infection.
XX
PS Disclosure; Page 54; 75pp; English.
XX
CC The present invention relates to a new gram-negative bacterial bleb
presenting on its surface the PorB outer membrane protein from Chlamydia
trachomatis, or a protective antigen from C. pneumoniae. The invention is
useful for preventing C. trachomatis or C. pneumoniae infection in a
host. The present amino acid sequence represents a Neisseria gonorrhoeae
protein as described in the invention
XX
SQ Sequence 174 AA;

Query Match 95.0%; Score 825; DB 5; Length 174;
Best Local Similarity 94.3%; Pred. No. 5.6e-82;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKYNKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 120
Db 61 FAVDYTRYKYNKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRRASHLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYVTPNVVDLDAGYRNYNIGKNTVTKNVRSGELSVGVVRVKF 174
Db 121 SKTSAGLGLVLAGVSAYVTPNVVDLDAGYRNYNIGKNTVTKNVRSGELSVGVVRVKF 174

RESULT 14
AAW04892
ID AAW04892 standard; protein; 175 AA.
XX
AC AAW04892;
XX
DT 16-OCT-2003 (revised)
DT 22-DEC-1996 (first entry)
XX
DE Proteinase K resistant N. meningitidis 22 kD surface protein.
XX
KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW antibody; detection; probe; surface protein.
XX
OS Neisseria meningitidis; strain MCH88.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= sig_peptide
FT Protein /label= mat_protein
XX
PN WO9629412-A1.
XX
PD 26-SEP-1996.
XX
PF 15-MAR-1996; 96WO-CA000157.
XX
PR 17-MAR-1995; 95US-00406362.
XX
PR 04-AUG-1995; 95US-0001983P.
XX
PA (IAFB-) IAF BIO VAC INC.
XX
PI Brodeur BR, Martin D, Hamel J, Rioux C;
XX
WPI; 1996-443187/44.
XX
N-PSDB; AAT39040.
XX
Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against, or
diagnosis of, N. meningitidis infection.
XX
Claim 7; Fig 8; 117pp; English.
XX
A proteinase K resistant surface protein has been isolated from 4 strains
of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
antigenic fragments of antibodies can be used in a vaccine for the
prevention of infection by N. meningitidis or by N. gonorrhoeae in
humans. The antibodies may also be used diagnostically to detect N.
meningitidis infection. The antigen may also be used to detect antibodies
specific to N. meningitidis antigen. DNA sequences encoding the antigen,
or their fragments, can be used as probes for the detection of pathogenic
CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 175 AA;

Query Match 95.0%; Score 824.5; DB 2; Length 175;
Best Local Similarity 95.4%; Pred. No. 6.4e-82;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
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Db 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDS 119  
Db 61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDS 120  
QY 120 FSQTSIGLGLTGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVRVKF 174  
Db 121 FSQTSIGLGLTGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVRVKF 175

RESULT 15  
ADL24385  
ID ADL24385 standard; protein; 166 AA.  
XX AC ADL24385;  
XX DT 03-JUN-2004 (first entry)  
XX DE N meningitidis strain 608B modified NspA protein #3.  
XX KW mutein; mutant; NspA; vaccine; antibacterial; meningitis.  
XX OS Neisseria meningitidis.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Misc-difference 35..36 /note= "wild-type NspA residues 36-43 deleted"  
XX WO2004019376-A2.

XX 11-MAR-2004.  
XX 29-AUG-2003; 2003WO-CA001452.  
XX 30-AUG-2002; 2002US-0406980P.  
XX (SHIR-) SHIRE BIOCHEM INC.  
XX Martin D, Rioux S;  
XX WPI; 2004-239123/22.  
XX Composition comprising liposome associated with isolated polypeptide or  
XX polynucleotide derived from Neisseria meningitidis strain 608B, or its  
XX fragment or analog, useful for inducing an immune response against N.  
XX meningitidis.

XX Example 4; Page; 79pp; English.  
XX The present invention relates to a pharmaceutical composition comprising  
XX a liposome associated with an isolated polypeptide derived from Neisseria  
XX meningitidis strain 608B, where the polypeptide is the NspA protein. The  
XX composition is useful for inducing an immune response against N.  
XX meningitidis, for preventing and/or treating N. meningitidis infection  
XX and for treating and/or preventing neisserial infection chosen from N.  
XX meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is  
XX useful for treatment or prophylaxis of meningitis and meningococcaemia, in  
XX a host. The host is a mammal, preferably a human and more preferably an  
XX adult human. The present sequence is a modified version of the Neisseria  
XX meningitidis strain 608B NspA protein. Note: This sequence is not shown  
XX in the specification but has been created based on the information given  
XX and the wild-type NspA protein shown in Figure 1.

XX Sequence 166 AA;  
XX Query Match 94.5%; Score 820; DB 8; Length 166;  
XX Best Local Similarity 95.4%; Pred. No. 1.8e-81;  
XX Matches 166; Conservative 0; Mismatches 0; Indels 8; Gaps 1;  
QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
|||||

Db 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAK-----KGFSPRISAGYRINDLR 52  
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 120  
Db 53 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 112  
QY 121 SQTSGIGLGLTGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVRVKF 174  
Db 113 SQTSGIGLGLTGVSYAVTPNVDLDAGYRYNYIGKNTVKNVRSGLSVGVVRVKF 166

Search completed: January 11, 2006, 15:18:36  
Job time : 79 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:15:42 ; Search time 40 Seconds  
(without alignments)  
418.543 Million cell updates/sec

Title: US-10-650-123-2  
Perfect score: 868  
Sequence: 1 MKKALATLIALPALPAALAE.....VNTKVRSGELSGVGRVKF 174  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	864	99.5	174	2 G81174	outer membrane pro
2	854	98.4	174	2 B81932	outer membrane pro
3	244.5	28.2	261	2 S16610	opacity protein op
4	242	27.9	260	2 S16611	opacity protein op
5	241.5	27.8	338	2 S16613	opacity protein op
6	241	27.8	258	2 S16612	opacity protein op
7	241	27.8	260	1 KONH0	opacity protein op
8	240.5	27.7	237	2 S36343	opacity protein op
9	240.5	27.7	257	2 S16614	opacity protein op
10	239	27.5	266	2 S16616	opacity protein op
11	238	27.4	258	2 S08514	opacity protein-re
12	237	27.3	254	2 S20043	opacity protein B
13	237	27.3	270	2 S04380	opacity protein P.
14	236.5	27.2	268	1 KONH2C	opacity protein P.
15	236	27.2	283	2 S72343	opacity protein op
16	232.5	26.8	234	2 S36329	opacity protein op
17	232.5	26.8	282	2 S16617	opacity protein op
18	232	26.7	234	2 S36342	opacity protein op
19	232	26.7	234	2 S36341	opacity protein op
20	231	26.6	233	2 S36350	opacity protein op
21	226	26.0	234	1 KONH8	opacity protein V2
22	226	26.0	234	2 S36348	opacity protein op
23	226	26.0	238	2 S36349	opacity protein op
24	226	26.0	261	2 S16619	opacity protein op
25	224.5	25.9	243	2 S36346	opacity protein op
26	221	25.5	248	2 P10038	opacity protein D
27	219	25.2	238	2 S36344	opacity protein ho
28	217	25.0	178	2 F64124	opacity protein ho
29	215	24.8	239	2 S28630	opacity protein op

30	205.5	23.7	247	2 S28627	opacity protein op
31	203.5	23.4	214	2 S44706	opacity protein op
32	189.5	21.8	235	2 S44707	opacity protein op
33	180	20.7	121	2 I64187	opacity protein ho
34	150.5	17.3	210	2 S77737	opacity protein op
35	141	16.2	187	2 S20044	opacity protein op
36	135	15.6	168	2 S08513	opacity protein-re
37	135	15.6	170	2 T10256	opacity protein-re
38	132	15.2	239	2 AH0541	probable outer mem
39	129.5	14.9	281	2 AH3012	outer surface prot
40	129.5	14.9	284	2 G98271	hypothetical prote
41	126.5	14.6	70	2 F64086	probable outer mem
42	126.5	14.6	201	2 S16286	opacity protein op
43	126	14.5	192	2 S44712	opacity protein op
44	122	14.1	284	2 AG3556	heat resistant agg
45	121.5	14.0	264	2 I54668	heat resistant agg

ALIGNMENTS

RESULT 1

G81174  
outer membrane protein Nega NMB0663 [imported] - Neisseria meningitidis (strain MC58 ser C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: G81174  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Rhee, G.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, C., Sun, L., Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: G81174  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-174 <TET>  
A:Cross-references: UNIPROT:Q9RP17; UNIPARC:UPI000000D41C1; GB:AE002420; GB:AE002098; NID A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0663

Query Match 99.5%; Score 864; DB 2; Length 174;

Best Local Similarity 99.4%; Pred. No. 6.9e-70;

Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Qy 121 SQTSGILGVLTVGSYAVTPNVVDLAGRYNYIGKVTNKVRSGELSGVGRVKF 174

Db 121 SQTSGILGVLTVGSYAVTPNVVDLAGRYNYIGKVTNKVRSGELSGVGRVKF 174

RESULT 2

B81932  
outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain Z2491 serogroup C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: B81932  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Nature 404, 502-506, 2000  
A:Authors: S. J. Achtman, M. James, K. D. Bentley, S. D. Churcher, C. Klee, S. R.; Morel A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491. A:Reference number: AB1775; MUID:20222556; PMID:10761919  
A:Accession: B81932  
A:Status: preliminary



A:Molecule type: DNA  
A:Residues: 1-174 <PAR>  
A:Cross-references: UNIPROT:P95372; UNIPARC:UPI00000D41C0; GB:AL1162754; GB:AL1157959; NID  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: nsPa; NMA0862

Query Match 98.4%; Score 854; DB 2; Length 174;  
Best Local Similarity 98.3%; Pred. No. 5.4e-69;  
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASALYDPTQSPVKPYLGARLSNRAVDLGGSDSF 120  
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASALYDPTQSPVKPYLGARLSNRAVDLGGSDSF 120

Qy 121 SQTSLGLVLTGVSVAVTPNVLDAGYRINYIGKNTVKNVRSGLSVGVVRVKF 174  
Db 121 SQTSLGLVLTGVSVAVTPNVLDAGYRINYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 3  
S16610  
opacity protein opaK precursor - Neisseria gonorrhoeae (strain MS11) (fragments)  
N:Alternate names: outer membrane protein opaK  
C:Species: Neisseria gonorrhoeae  
A:Variety: strain MS11  
C:Date: 13-Jan-1995 #sequence\_revision 17-Oct-1997 #text\_change 17-Oct-1997  
C:Accession: S16610  
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1989-1901, 1991  
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein  
A:Reference number: S16610; MUID:92114767; PMID:1815562  
A:Accession: S16610  
A:Molecule type: DNA  
A:Residues: 1-261 <BHA>  
A:Cross-references: UNIPARC:UPI0000178215; EMBL:X52364  
A:Experimental source: strain MS11, variant 4.8  
A:Note: the authors did not translate the sequence for the signal peptide  
A:Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein  
C:Genetics:  
A:Gene: opaK  
C:Superfamily: opacity protein  
C:Keywords: cell surface component; transmembrane protein  
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
F:24-261/Product: opacity protein opaK #status predicted <MAT>  
F:34-42/Domain: transmembrane #status predicted <TM1>  
F:43-75/Domain: extracellular #status predicted <EXT1>  
F:51-61/Region: semivariable region  
F:76-84/Domain: transmembrane #status predicted <TM2>  
F:89-95/Domain: transmembrane #status predicted <TM3>  
F:96-134/Domain: extracellular #status predicted <EXT2>  
F:102-129/Region: hypervariable region HV1  
F:135-149/Domain: transmembrane #status predicted <TM4>  
F:155-165/Domain: transmembrane #status predicted <TM5>  
F:166-212/Domain: extracellular #status predicted <EXT3>  
F:171-218/Region: hypervariable region HV2  
F:213-225/Domain: transmembrane #status predicted <TM6>  
F:229-237/Domain: transmembrane #status predicted <TM7>  
F:239-252/Domain: extracellular #status predicted <EXT4>  
F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 28.2%; Score 244.5; DB 2; Length 261;  
Best Local Similarity 29.9%; Pred. No. 1.9e-14;  
Matches 73; Conservative 26; Mismatches 59; Indels 87; Gaps 10;

Qy 15 AAALAEAG-ASGFYVQADAAHAKA-----SSLSGSAKG-----FSPRI 50  
Db 21 AQAASEGNGRGPYVQADLAAEAERITHDYPTGAKGTTISTVSDYFRNIRTHSIHPRV 80

Qy 51 SAGYRINDLRFAVDYTRYKNY-----KAPSTDFK-----LYS 82  
Db 81 SVGVDFGWRIAADYARYKRWNNNKYSVSIKELLRNKNGNRITDLKAENQENGTFHAVSS 140

Qy 83 IGASAIYDFTQSPVKPYLGARLSN--RASVD-----LGG----- 116  
Db 141 LGLSAVYDFKLNDFKFPYIGARVAIGHVRSIDSTKTKTEVTTLHGFGTTPTVYPGKNT 200

Qy 117 -----SDFSQTSIGLGLTGVSVAVTPNVLDAGYRINYIGKNTVKNVRSGLSVGV 170  
Db 201 QNAHRESDSIRR--VGLGAVAGVGDITPNTLDAGYRINYGRLENT-RFKTHEASLGV 257

Qy 171 RVKF 174  
Db 258 RYRP 261

RESULT 4  
S16611  
opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments)  
N:Alternate names: outer membrane protein opa58  
C:Species: Neisseria gonorrhoeae  
A:Variety: strain MS11  
C:Date: 04-Jun-1997 #sequence\_revision 17-Oct-1997 #text\_change 09-Jul-2004  
C:Accession: S16611; S36345; S28624  
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1989-1901, 1991  
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein  
A:Reference number: S16610; MUID:92114767; PMID:1815562  
A:Accession: S16611  
A:Molecule type: DNA  
A:Residues: 1-260 <BHA>  
A:Cross-references: UNIPROT:Q04882; UNIPARC:UPI00001781FE; EMBL:X52371  
A:Experimental source: strain MS11, variant 4.8  
A:Note: the authors did not translate the sequence for the signal peptide  
A:Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein  
R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.P. EMBO J. 12, 641-650, 1993  
A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di  
A:Reference number: S36328; MUID:93178439; PMID:8440254  
A:Accession: S36345  
A:Molecule type: DNA  
A:Residues: 24-260 <KUP>  
A:Cross-references: UNIPARC:UPI0000130D60; EMBL:Z18937; NID:G49333; PIDN:CAA79370.1; PID  
A:Experimental source: strain MS11, variant F3  
A:Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein  
C:Genetics:  
A:Gene: opaJ  
C:Superfamily: opacity protein  
C:Keywords: cell surface component; transmembrane protein  
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
F:24-260/Product: opacity protein opaJ #status predicted <MAT>  
F:34-42/Domain: transmembrane #status predicted <TM1>  
F:43-74/Domain: extracellular #status predicted <EXT1>  
F:51-60/Region: semivariable region  
F:75-83/Domain: transmembrane #status predicted <TM2>  
F:88-94/Domain: transmembrane #status predicted <TM3>  
F:95-133/Domain: extracellular #status predicted <EXT2>  
F:101-128/Region: hypervariable region HV1  
F:134-148/Domain: transmembrane #status predicted <TM4>  
F:154-164/Domain: transmembrane #status predicted <TM5>  
F:165-211/Domain: extracellular #status predicted <EXT3>  
F:170-217/Region: hypervariable region HV2  
F:212-224/Domain: transmembrane #status predicted <TM6>  
F:228-236/Domain: transmembrane #status predicted <TM7>  
F:237-251/Domain: extracellular #status predicted <EXT4>  
F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.9%; Score 242; DB 2; Length 260;  
Best Local Similarity 29.5%; Pred. No. 3.2e-14;

```
Matches 76; Conservative 27; Mismatches 67; Indels 88; Gaps 10;
QY 2 KKALATLIALALPAALAEAG---ASGFYVQADAHA-----KASSSLGSAGKFS- 47
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 KKPSSLFSSLLPSSAAQAAGEDHGRGPYVQADLAYAYEHI THDYPEQTDPSKGKISTVSD 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 48 -----PRISAGYRINDLRPAVDYTRYKN-----KAPSTDPK 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 YFRNIRTHSIHPRVSVGVDFGWRIAADYARYRKNNKNSYSIKELLRNKNGNRTDRK 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 -----LYSTGASAIYDFTQSPVKPYLGARLSLN--RASVD-----LG 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 TENQNGTFAVSSGLSAVDYKLNDFKFPYIGARVAYGHVHRHSIDSTKTKTEVTTLH 185
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 G-----SDSFQTSIGLGLVATGVSVAVTNPVLDLAGYRYNYIGKVN 156
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 GPGTTPVYVPGKNTQDAHRESDSIRR--VGLGAVAGVGIDITPNTLTDAGYRYHYWGRLE 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 157 TVKNVRSGLSVGVKVF 174
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 NTR-EKTHEASLGVRYP 260
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
SI6613
opacity protein opaB precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: SI6613
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,
Mol. Microbiol. 5, 1889-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A:Reference number: SI6610; MUID:92114767; PMID:1815562
A:Accession: SI6613
A:Molecule type: DNA
A:Residues: 1-338 <BHA>
A:Cross-references: UNIPARC:UPI0000178200; EMBL:X52373
A:Experimental source: strain MS11, variant 4.8
A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaB
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-13,14-104/Domain: signal sequence (fragments) #status predicted <SIG>
F:105-338/Product: opacity protein opaB #status predicted <MAT>
F:115-123/Domain: transmembrane #status predicted <TM1>
F:124-155/Domain: extracellular #status predicted <EXT1>
F:132-141/Region: semivariable region
F:156-164/Domain: transmembrane #status predicted <TM2>
F:169-175/Domain: transmembrane #status predicted <TM3>
F:176-212/Domain: extracellular #status predicted <EXT2>
F:182-207/Region: hypervariable region HV1
F:213-227/Domain: transmembrane #status predicted <TM4>
F:224-289/Domain: extracellular #status predicted <EXT3>
F:233-243/Domain: transmembrane #status predicted <TM5>
F:249-Region: hypervariable region HV2
F:290-302/Domain: transmembrane #status predicted <TM6>
F:306-314/Domain: transmembrane #status predicted <TM7>
F:315-329/Domain: extracellular #status predicted <EXT4>
F:330-338/Domain: transmembrane #status predicted <TM8>

Query Match 27.8%; Score 241.5; DB 2; Length 338;
Best Local Similarity 30.0%; Pred. No. 4.9e-14;
Matches 73; Conservative 25; Mismatches 66; Indels 79; Gaps 9;
QY 10 ALALPAALAEAG-ASGFYVQADAHA-----KASSSLGS-----AKGP 46
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 97 SLLFAARAESENGRGPYVQADLAYAABRITHDYPEPTGAKDKKSTVSDYFRNIRTHSI 156
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 47 SPRISAGYRINDLRPAVDYTRYK--NYKAPSTDPK-----L 80
```

```
Db 157 HPRVSVGVDFGWRIAADYARYRKNNKNSYDIKELENKNNKEDLKTENQENGTFHAY 216
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 81 YSIGASAIYDFTQSPVKPYLGARLSLN--RASVD-----LGG----- 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 217 SSLGLSAVDYKLNDFKFPYIGARVAYGHVHRHSIDSTKTKYKFLTSSVGLNPTVYTEEN 276
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 -----SDSFQTSIGLGLVATGVSVAVTNPVLDLAGYRYNYIGKVNTRVRSGLSVGR 171
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 277 TONAHQNSIRRVGLGIAGVGPDITPKLTLDTCYRYHYWGRLENTR-EKTHEASLGVR 335
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 172 VKF 174
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 336 YRF 338
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
SI6612
opacity protein opaE precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: SI6612
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,
Mol. Microbiol. 5, 1889-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami
A:Reference number: SI6610; MUID:92114767; PMID:1815562
A:Accession: SI6612
A:Molecule type: DNA
A:Residues: 1-258 <BHA>
A:Cross-references: UNIPARC:UPI00001781FD; EMBL:X52369
A:Experimental source: strain MS11, variant 4.8
A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaE
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-258/Product: opacity protein opaE #status predicted <MAT>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-74/Domain: extracellular #status predicted <EXT1>
F:50-60/Region: semivariable region
F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>
F:95-131/Domain: extracellular #status predicted <EXT2>
F:101-125/Region: hypervariable region HV1
F:132-146/Domain: transmembrane #status predicted <TM4>
F:152-162/Domain: transmembrane #status predicted <TM5>
F:163-209/Domain: extracellular #status predicted <EXT3>
F:168-215/Region: hypervariable region HV2
F:210-222/Domain: transmembrane #status predicted <TM6>
F:226-234/Domain: transmembrane #status predicted <TM7>
F:235-249/Domain: extracellular #status predicted <EXT4>
F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match 27.8%; Score 241; DB 2; Length 258;
Best Local Similarity 29.7%; Pred. No. 3.9e-14;
Matches 76; Conservative 26; Mismatches 68; Indels 86; Gaps 10;
QY 2 KKALATLIALALPAALAEAG---ASGFYVQADAHA-----KASSSLGSAK----- 44
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 KKPSSLFSSLLPSSAAQAAGEDHGRGPYVQADLAYAYEHI THDYPEPTGKDKKISTVSD 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 45 -----GFSFPRISAGYRINDLRPAVDYTRYK--NYKAPSTDPK----- 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 YFRNIRTHSIHPRVSVGVDFGWRIAADYARYRKNNKNSYDIKELENKNNKEDLKTKE 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 -----LYSIGASAIYDFTQSPVKPYLGARLSLN--RASVD-----LGG- 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 NOENGTFAVSSGLSAVDYKLNDFKFPYIGARVAYGHVHRHSIDSTKTKTEVTTLHGP 185
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```







R;Palmer, L.; Brooks, G.F.; Falkow, S.  
Mol. Microbiol. 3, 663-671, 1989  
A;Title: Expression of gonococcal protein II in *Escherichia coli* by translational fusion  
A;Reference number: S04380; MUID:89343653; PMID:2503682  
A;Accession: S04380  
A;Molecule type: DNA  
A;Residues: 1-270 <PAL>  
A;Cross-references: UNIPROT:Q50959; UNIPARC:UPI000017821A; EMBL:X15780  
A;Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1  
A;Note: the authors did not translate the sequence of the signal peptide  
A;Note: expression of opacity proteins is regulated by the number of translated repeat  
of repeats place the start codon in frame with the rest of the protein  
R;Tana, M.K.; So, M.; Seifert, H.S.; Billyard, E.; Marchal, C.  
EMBO J. 7, 4367-4378, 1988  
A;Title: Pilin expression in *Neisseria gonorrhoeae* is under both positive and negative  
A;Reference number: S02017; MUID:89210824; PMID:2854063  
A;Accession: S16504  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 259-270 <TAH>  
A;Cross-references: UNIPARC:UPI00000AF0FB; EMBL:X13965  
A;Experimental source: strain M511A  
A;Note: expression of opacity proteins is regulated by the number of translated repeat  
of repeats place the start codon in frame with the rest of the protein  
C;Genetics:  
A;Gene: opaB1  
C;Keywords: cell surface component; transmembrane protein  
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
F;24-270/Product: opacity protein opaK #status predicted <MAT>  
F;34-42/Domain: transmembrane #status predicted <TM1>  
F;43-75/Domain: extracellular #status predicted <EXT1>  
F;51-61/Region: semivariable region  
F;76-84/Domain: transmembrane #status predicted <TM2>  
F;89-95/Domain: transmembrane #status predicted <TM3>  
F;96-141/Domain: extracellular #status predicted <EXT2>  
F;102-136/Region: hypervariable region HV1  
F;142-156/Domain: transmembrane #status predicted <TM4>  
F;162-172/Domain: transmembrane #status predicted <TM5>  
F;173-221/Domain: extracellular #status predicted <EXT3>  
F;178-227/Region: hypervariable region HV2  
F;222-234/Domain: transmembrane #status predicted <TM6>  
F;238-246/Domain: transmembrane #status predicted <TM7>  
F;247-261/Domain: extracellular #status predicted <EXT4>  
F;262-270/Domain: transmembrane #status predicted <TM8>

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Best Local Similarity 27.1%; Pred. No. 9.4e-14;  
Matches 72; Conservative 33; Mismatches 67; Indels 94; Gaps 8;  
QY 2 KKALATLALPAALAEAG---ASGFYVQADAAH-----AKASSLSGSAK 44  
DB 6 KKPSSLFSSLLPSSAAQAAGEGNGPGPVQADLAYAVEHITHDYPKPTGAKKGTITSVS 65  
QY 45 GF-----SPRISAGYRINDLPAVDYTRYK----- 69  
DB 66 DYFRNIRTHSVHPRVSVGYDFGFWRIAADYARYKNNNNKYSVSIKELGRNDSASGVRG 125  
QY 70 --NYKAPSTDFK-----LYSIGASAIYDFTQSPVKPYLGARLSL----- 107  
DB 126 HLNITQKTEHQENGTFHAASLSGLSTIYDFTGSRFPKPYIGARVAYGHVRHQRVSVEQE 185  
QY 108 -----NRASVDLGGSS-----DSFQTSISGLVLTGVSVAFTPNVDLDAGYR 148  
DB 186 TEIVTTPYKEQNVAPSPIPGAPTKKPAHBSRSISLFGAVAGVIGDITNLTLDAGYR 245  
QY 149 YNYIGKVNTRKVRSGELSVGVRVKF 174  
DB 246 YHNWGRLENTNTR-FKTHEASLGVRVRF 270

RESULT 14  
KONH2C  
opacity protein P.IIc precursor - *Neisseria gonorrhoeae* (strain JS3) (fragments)

N;Alternate names: outer membrane protein P.IIc  
C;Species: *Neisseria gonorrhoeae*  
A;Variety: strain JS3  
C;Date: 31-Mar-1992 #sequence\_revision 17-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S03095; S16360  
R;van der Ley, P.  
Mol. Microbiol. 2, 797-806, 1988  
A;Title: Three copies of a single protein II-encoding sequence in the genome of *Neisseria*  
A;Reference number: S03095; MUID:89096501; PMID:3145386  
A;Accession: S03095  
A;Molecule type: DNA  
A;Residues: 1-268 <VAN>  
A;Cross-references: UNIPROT:P09888; UNIPARC:UPI00001747E4; EMBL:X12625  
A;Experimental source: strain JS3  
A;Note: 241-Val was also found  
A;Note: expression of opacity proteins is regulated by the number of translated repeat  
of repeats place the start codon in frame with the rest of the protein  
R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.  
Infect. Immun. 55, 2026-2031, 1987  
A;Title: Antigenic and structural differences among six proteins II expressed by a single  
A;Reference number: S16360; MUID:87306843; PMID:3114142  
A;Accession: S16360  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 24-34 <BAR>  
A;Cross-references: UNIPARC:UPI00001747E5  
C;Genetics:  
A;Gene: pilC  
C;Superfamily: opacity protein  
C;Keywords: cell surface component; transmembrane protein  
F;1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
F;24-268/Product: opacity protein P.IIc #status experimental <MAT>  
F;34-42/Domain: transmembrane #status predicted <TM1>  
F;43-74/Domain: extracellular #status predicted <EXT1>  
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F;75-83/Domain: transmembrane #status predicted <TM2>  
F;88-94/Domain: transmembrane #status predicted <TM3>  
F;95-140/Domain: extracellular #status predicted <EXT2>  
F;101-135/Region: hypervariable region HV1  
F;141-155/Domain: transmembrane #status predicted <TM4>  
F;161-171/Domain: transmembrane #status predicted <TM5>  
F;172-219/Domain: extracellular #status predicted <EXT3>  
F;177-225/Region: hypervariable region HV2  
F;220-232/Domain: transmembrane #status predicted <TM6>  
F;236-244/Domain: transmembrane #status predicted <TM7>  
F;245-259/Domain: extracellular #status predicted <EXT4>  
F;260-268/Domain: transmembrane #status predicted <TM8>

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Best Local Similarity 26.8%; Pred. No. 1e-13;  
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QY 6 ATLIALPALPAALAEAGSGFYVQADAAHAKA-----SSSLSGSAK----- 44  
DB 13 SLLLFSSAAARAAASDGGGPGPVQADLAYAERIITHDYPKPTGKKNKISTVSDYFRNIRT 72  
QY 45 -GFSPRISAGYRINDLPAVDYTRYK-----NYKAPS 75  
DB 73 HSHVHPRVSVGYDFGFWRIAADYARYKNNNNKYSVSIKELGRNDSASGVRGHLNIQTOK 132  
QY 76 TDFK-----LYSIGASAIYDFTQSPVKPYLGARLSLRA-----SVDL----- 114  
DB 133 TEHQENGTFHVASLSGLSTIYDFTGSRFPKPYIGARVAYGHVRHQRVSVEQETETITTPY 192  
QY 115 ---CGSDSPFSQ-----TSIGLGLVLTGVSVAFTPNVDLDAGYRNYIGKVN 157  
DB 193 SNGGKRVSLSSKMPKSAHQNSIRRVGLGLVGIAGVGPDITPNLTLDGTGYRHNWGRLEN 252  
QY 158 VKNVRSGELSVGVRVKF 174  
DB 253 TR-FKTHEASLGVRVRF 268



RESULT 15  
S72343  
opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)  
N:Alternate names: cell invasion protein opaH  
C:Species: Neisseria gonorrhoeae  
A:Variety: isolate 15063G  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S72343  
Mol. Microbiol. 13, 919-928, 1994  
R:Waldbeser, L.S.; Ajioka, R.S.; Merz, A.J.; Puaoli, D.; Lin, L.; Thomas, M.; So, M.  
A:Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell invasion  
A:Reference number: S72343; MUID:95115561; PMID:7815949  
A:Accession: S72343  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-283 <WAL>  
A:Cross-references: UNIPROT:Q50943; UNIPARC:UPI00000BB96E; EMBL:U13708; NID:G535357; PID:15063G  
A:Experimental source: isolate 15063G  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
A:Note: expression of opacity proteins is regulated by the number of translated repeats of repeats place the start codon in frame with the rest of the protein  
C:Superfamily: opacity protein  
C:Keywords: cell surface component; transmembrane protein  
F:1-48/Domain: signal sequence #status predicted <SIG>  
F:49-283/Product: opacity protein opaH #status predicted <MAT>  
F:58-66/Domain: transmembrane #status predicted <TM1>  
F:67-98/Domain: extracellular #status predicted <EXT1>  
F:75-84/Region: semivariable region  
F:99-107/Domain: transmembrane #status predicted <TM2>  
F:112-118/Domain: transmembrane #status predicted <TM3>  
F:119-155/Domain: extracellular #status predicted <EXT2>  
F:125-150/Region: hypervariable region HV1  
F:156-170/Domain: transmembrane #status predicted <TM4>  
F:176-186/Domain: transmembrane #status predicted <TM5>  
F:187-234/Domain: extracellular #status predicted <EXT3>  
F:192-240/Region: hypervariable region HV2  
F:235-247/Domain: transmembrane #status predicted <TM6>  
F:251-259/Domain: transmembrane #status predicted <TM7>  
F:260-274/Domain: extracellular #status predicted <EXT4>  
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Query Match 27.2%; Score 236; DB 2; Length 283;  
Best Local Similarity 27.9%; Pred. NO. 1.2e-13;  
Matches 68; Conservative 29; Mismatches 67; Indels 80; Gaps 7;  
Qy 10 ALALPAALAEAGSGFYQDAAHAKA-----SSSLGSAGK-----FS 47  
Db 41 SLLSAAQAASEAMRGFYQDAFAAERITHDYPEPTGKKGITSTVSDYFRNIRTHSVH 100  
Qy 48 PRISAGYRINDLRPAVDYTRYKNY-----KAPS-----TDPKLY 81  
Db 101 PRVSVGYDFGGRWIRADYARFKNNKYNKYNIRVQEAHNSRIDLKAENQENGTFHVS 160  
Qy 82 SIGASAIYDFDTQSPVKPYLGARLSN--RASVDL----- 114  
Db 161 SLGLSAVYDFKLNDFKFIYGARVAYGHVRHSIDSTKTKILTSTFYGVATKPTTYDIGP 220  
Qy 115 -----GGSDSFQSTGIGLVLTGVSVAVTPNVDDLADAGRYNYIKVNTVKNVRSGLSVGV 170  
Db 221 KTDQAHOESNSIRRVGLGVGIAGVGFDITPKLTLDGTGYRHYWGRLENTF-EKTHEASLGM 279  
Qy 171 RVKF 174  
Db 280 RYRP 283

Search completed: January 11, 2006, 15:22:19  
Job time : 41 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 11, 2006, 15:14:46 ; Search time 161 Seconds  
(without alignments)  
762.496 Million cell updates/sec

Title: US-10-650-123-2  
Perfect score: 868  
Sequence: 1 MKKALATLIALPALAALAE.....VNTKVRSGELSGVRVKF 174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2	P96943 NEIME
2	864	99.5	174	2	Q9P17 NEIME
3	864	99.5	174	2	Q7DDM2 NEIME
4	857	98.7	174	2	Q9R2R1 NEIME
5	854	98.4	174	2	P95372 NEIME
6	854	98.4	174	2	Q7AR60 NEIME
7	852	98.2	174	2	Q9P18 NEIME
8	846	97.5	174	2	P95343 NEIME
9	825	95.0	175	2	P95371 NEIME
10	824.5	95.0	175	2	Q9FA01 NEIME
11	809.5	93.3	175	2	Q65RV6 MANSUM
12	303.5	35.0	226	2	Q65TE2 MANSUM
13	256	29.5	226	2	Q51124 NEIME
14	247	28.5	256	2	Q9CM19 PASMU
15	246.5	28.4	186	2	Q9R719 NEIME
16	244	28.1	234	2	Q07280 NEIME
17	244	28.1	234	2	Q9R718 NEIME
18	243	28.0	234	2	Q9PAJ NEIME
19	242	27.9	260	1	Q9K4T9 NEIME
20	241.5	27.8	232	2	Q9AE80 NEIME
21	241.5	27.8	241	2	Q9R9A7 NEIME
22	240.5	27.7	230	2	Q9R9A7 NEIME
23	240.5	27.7	237	1	Q9AK NEIME
24	240	27.6	241	2	Q9K4T4 NEIME
25	240	27.6	259	2	Q51126 NEIME
26	240	27.6	259	2	Q51125 NEIME
27	239.5	27.6	232	2	Q9R3P5 NEIME
28	239	27.5	260	1	Q9R1 NEIME
29	238.5	27.5	257	2	Q50929 NEIME
30	238	27.4	234	2	Q07287 NEIME
31	238	27.4	237	2	Q31176 NEIME

RESULT 1

P96943 NEIME

ID P96943 NEIME PRELIMINARY; PRT; 174 AA.

AC P96943;

DT 01-MAY-1997 (Tremblrel. 03, Created)

DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)

DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

DE Outer membrane protein precursor (Surface protein A).

GN Name=nsa;

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI\_TaxID=487;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=608B;

RX MEDLINE=97253610; PubMed=9104804; DOI=10.1084/jem.185.7.1173;

RA Martin D., Cadieux N., Hamel J., Brodeur B.R.;

RT "Highly conserved Neisseria meningitidis surface protein confers

RT protection against experimental infection.";

RL J. Exp. Med. 185:1173-1183(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=608B;

RX MEDLINE=99270944; PubMed=10338491;

RA Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;

RT "Antigenic and molecular conservation of the gonococcal NspA

RT protein.";

RL Infect. Immun. 67:2855-2861(1999).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=608B;

RX MEDLINE=99386904; PubMed=10456958;

RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;

RT "Bactericidal and cross-protective activities of a monoclonal antibody

RT directed against Neisseria meningitidis NspA outer membrane protein.";

RL Infect. Immun. 67:4955-4959(1999).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=M986, NG6/88, and NGP165;

RA Moe G.R., Tan S., Granoff D.M.;

RT "Differences in Surface Expression of Neisserial Surface Protein A

RT among Neisseria meningitidis Group B strains.";

RL Infect. Immun. 0:0-0(1999).

DR EMBL; U52066; AAC36000.1; -; Genomic DNA.

DR EMBL; AF175680; AADS3283.1; -; Genomic DNA.

DR EMBL; AF175682; AADS3285.1; -; Genomic DNA.

DR EMBL; AF175683; AADS3286.1; -; Genomic DNA.

DR HSSP; Q9RP17; 1P4T.

DR SMR; P96943; 20-174.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0015288; F:porin activity; IEA.

DR InterPro; IPR003394; Porin\_opacity.

DR Pfam; PF02462; Opacity; 1.

DR

DR

DR

DR

DR

DR

DR

DR

KW Signal.  
 FT SIGNAL 1 19 Potential.  
 SQ SEQUENCE 174 AA; 18425 MW; E8B02767DDC6FEL9 CRC64;

Query Match 100.0%; Score 868; DB 2; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-69;  
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRSASVDLGGSDSF 120  
 DB 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRSASVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174  
 DB 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174

RESULT 3  
 Q9RP17\_NEIME  
 ID Q9RP17\_NEIME PRELIMINARY; PRT; 174 AA.  
 AC Q9RP17;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Surface protein A.  
 GN Name=nsa;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CU385;  
 RA Moe G.R., Tan S., Granoff D.M.;  
 RT "Differences in Surface Expression of Neisserial Surface Protein A  
 among Neisseria meningitidis Group B strains.";  
 RL Infect. Immun. 0:0-0(1999).  
 DR EMBL; AF175678; AAD53281.1; -; Genomic\_DNA.  
 DR PIR; G81174; G81174.  
 DR PDB; 1P4T; X-ray; A=20-174.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0015288; F:porin activity; IEA.  
 DR InterPro; IPR003394; Porin:opacity.  
 DR Pfam; PF02462; Opacity; 1.  
 SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-68;  
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 ID Q7DDM2\_NEIME PRELIMINARY; PRT; 174 AA.  
 AC Q7DDM2;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Outer membrane protein NspA.  
 GN Name=nsa; OrderedLocName=NMB0663;  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=491;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MC58 / Serogroup B;  
 MEDLINE=20175755; Pubmed=10710307; DOI=10.1126/science.287.5459.1809;  
 RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,  
 RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,  
 RA Dickson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,  
 RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,  
 RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,  
 RA Clifton H., Clark E.B., Cotton M.D., Ueberback T.R., Khouri H.M.,  
 RA Qin H., Vamathevan J.J., Gill J., Scariato V., Maignani V., Pizzo M.,  
 RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,  
 RA Venter J.C.;  
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
 MC58";  
 RL Science 287:1809-1815(2000).  
 DR EMBL; AE002098; AAF410R1.1; -; Genomic\_DNA.  
 DR SMR; Q7DDM2; 20-174.  
 DR TIGR; NMB0663; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0015288; F:porin activity; IEA.  
 DR InterPro; IPR003394; Porin:opacity.  
 DR Pfam; PF02462; Opacity; 1.  
 DR Complete proteome.  
 SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-68;  
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QY 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRSASVDLGGSDSF 120  
 DB 61 FAVDTYTRYKYNKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRSASVDLGGSDSF 120

QY 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174  
 DB 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKVTNKVRSGLSVGVVRKF 174

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 AC Q9R2R1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Surface protein A.  
 GN Name=nsa;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=M136, and B232;  
 RA Moe G.R., Tan S., Granoff D.M.;  
 RT "Differences in Surface Expression of Neisserial Surface Protein A  
 among Neisseria meningitidis Group B strains.";  
 RL Infect. Immun. 0:0-0(1999).  
 DR EMBL; AF175679; AAD53282.1; -; Genomic\_DNA.  
 DR EMBL; AF175677; AAD53280.1; -; Genomic\_DNA.  
 DR HSP; Q9RP17; 1P4T.

DR SMR; Q9R2R1; 20-174.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR003394; Porin activity; IEA.  
 DR Pfam; PF02462; Opacity; 1.  
 SQ SEQUENCE 174 AA; 18395 MW; ECF6F39A9286910E CRC64;  
 Query Match 98.7%; Score 857; DB 2; Length 174;  
 Best Local Similarity 98.3%; Pred. No. 7.8e-68;  
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 Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 Qy 121 SQTSGIGLVLTGVSVAVTPNVLDLAGYRNYIGKVTNKVRSGLSVGVVRKF 174  
 Db 121 SQTSGIGLVLTGVSVAVTPNVLDLAGYRNYIGKVTNKVRSGLSVGVVRKF 174

RESULT 5  
 ID P95372 NEIME PRELIMINARY; PRT; 174 AA.  
 AC P95372;  
 DT 01-MAY-1997 (TremBLrel. 03, Created)  
 DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)  
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
 DE Outer membrane protein precursor.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OK NCBI\_TaxID=487;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Z4063;  
 RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;  
 RT "Bactericidal and cross-protective activities of a monoclonal antibody  
 directed against Neisseria meningitidis NspA outer membrane protein.";  
 RL Infect. Immun. 67:4955-4959(1999).  
 DR EMBL; U52068; AAB41580.1; -; Genomic\_DNA.  
 DR PIR; B81932; B81932.  
 DR HSP; Q9RP17; 1P4T.  
 DR SMR; P95372; 20-174.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR003394; Porin activity; IEA.  
 DR Pfam; PF02462; Opacity; 1.  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;  
 Query Match 98.4%; Score 854; DB 2; Length 174;  
 Best Local Similarity 98.3%; Pred. No. 1.4e-67;  
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 Qy 121 SQTSGIGLVLTGVSVAVTPNVLDLAGYRNYIGKVTNKVRSGLSVGVVRKF 174  
 Db 121 SQTSGIGLVLTGVSVAVTPNVLDLAGYRNYIGKVTNKVRSGLSVGVVRKF 174

RESULT 6  
 Q7AR60 NEIMA PRELIMINARY; PRT; 174 AA.  
 AC Q7AR60;  
 DT 05-JUL-2004 (TremBLrel. 27, Created)  
 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)  
 DE Outer membrane protein.  
 GN Name=nsa; OrderedLocuNames=NMA0862;  
 OS Neisseria meningitidis (serogroup A).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OK NCBI\_TaxID=65699;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;  
 RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,  
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,  
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,  
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 RA Whitehead S., Spratt B.G., Barrell B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria  
 meningitidis Z2491."  
 RL Nature 404:502-506(2000).  
 DR EMBL; AL162754; CAB84143.1; -; Genomic\_DNA.  
 DR SMR; Q7AR60; 20-174.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0015288; F:porin activity; IEA.  
 DR InterPro; IPR003394; Porin opacity.  
 DR Pfam; PF02462; Opacity; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match 98.4%; Score 854; DB 2; Length 174;  
 Best Local Similarity 98.3%; Pred. No. 1.4e-67;  
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDSF 120  
 Qy 121 SQTSGIGLVLTGVSVAVTPNVLDLAGYRNYIGKVTNKVRSGLSVGVVRKF 174  
 Db 121 SQTSGIGLVLTGVSVAVTPNVLDLAGYRNYIGKVTNKVRSGLSVGVVRKF 174

RESULT 7  
 Q9RP16 NEIME PRELIMINARY; PRT; 174 AA.  
 AC Q9RP16;  
 DT 01-MAY-2000 (TremBLrel. 13, Created)  
 DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
 DE Surface protein A.  
 GN Name=nsa;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OK NCBI\_TaxID=487;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NG3/88;  
 RA Moe G.R., Tan S., Granoff D.M.;  
 RT "Differences in Surface Expression of Neisserial Surface Protein A  
 among Neisseria meningitidis Group B strains.";  
 RL Infect. Immun. 0:0-0(1999).  
 DR EMBL; AF175681; AAD53284.1; -; Genomic\_DNA.

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DR HSSP; Q9RP17; 1P4T.
DR SMR; Q9RP16; 20-174.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;

Query Match 98.2%; Score 852; DB 2; Length 174;
Best Local Similarity 97.7%; Pred. No. 2.2e-67;
Matches 170; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Dy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Dy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Qy 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Dy 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 8
Q9RP18_NEIME
ID Q9RP18_NEIME PRELIMINARY; PRT; 174 AA.
AC Q9RP18;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface protein A.
GN Name=nsa;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8047;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175676; AA053279.1; -; Genomic_DNA.
DR HSSP; Q9RP17; 1P4T.
DR SMR; Q9RP18; 20-174.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18357 MW; 0205AA1DA1B7F005 CRC64;

Query Match 97.5%; Score 846; DB 2; Length 174;
Best Local Similarity 97.1%; Pred. No. 7.3e-67;
Matches 169; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Dy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Dy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Qy 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Dy 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 9
P95343_NEIGO
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ID P95343_NEIGO PRELIMINARY; PRT; 174 AA.
AC P95343;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Outer membrane protein precursor (Surface protein A).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2;
RX MEDLINE=99270944; PubMed=10338491;
RA Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
RT "Antigenic and molecular conservation of the gonococcal NspA
protein.";
RL Infect. Immun. 67:2855-2861(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WHO-A;
RX Mingchun J.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U52069; AAB41581.1; -; Genomic_DNA.
DR EMBL; AY157539; AAN77898.1; -; Genomic_DNA.
DR HSSP; Q9RP17; 1P4T.
DR SMR; P95343; 20-174.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 174 AA; 18337 MW; 1B558EC8A040841A CRC64;

Query Match 95.0%; Score 825; DB 2; Length 174;
Best Local Similarity 94.3%; Pred. No. 5.3e-65;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Dy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Dy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Qy 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Dy 121 SQTSGIGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 10
P95371_NEIME
ID P95371_NEIME PRELIMINARY; PRT; 175 AA.
AC P95371;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer membrane protein precursor.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MCH 88;
RX MEDLINE=99386904; PubMed=10456958;
RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
RT "Bactericidal and cross-protective activities of a monoclonal antibody
directed against Neisseria meningitidis NspA outer membrane protein.";
RL Infect. Immun. 67:4955-4959(1999).
DR EMBL; U52067; AAB41579.1; -; Genomic_DNA.
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DR HSP; Q9RPI7; 1P4T.
DR SMR; P95371; 20-175.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR0015288; F:porin activity; IEA.
DR Pfam; PF02462; Opacity; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 175 AA; 18572 MW; D1EA8P2FP5CC2FEA CRC64;

Query Match 95.0%; Score 824.5; DB 2; Length 175;
Best Local Similarity 95.4%; Pred. No. 5.9e-65;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYK-APSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 119
Db 61 FAVDYTRYKNYKQVPSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 120

Qy 120 FQSTSIGGLVLTGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGRVKF 174
Db 121 FQSTSTGLGLAGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGRVKF 175

RESULT 11
Q5FA01_NEIG1 PRELIMINARY; PRT; 175 AA.
AC Q5FA01;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Outer membrane protein.
GN OrderedLocusNames=NG002333;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaspay A.P., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ownbey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004969; AAW88986.1; -; Genomic_DNA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Complete proteome.
SQ SEQUENCE 175 AA; 18478 MW; 44C05922D87FACF8 CRC64;

Query Match 93.3%; Score 809.5; DB 2; Length 175;
Best Local Similarity 93.1%; Pred. No. 1.3e-63;
Matches 163; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYK-APSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 119
Db 61 FAVDYTRYKNYKQVPSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 120

Qy 120 FQSTSIGGLVLTGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGRVKF 174
Db 121 FSKTSAGLGLAGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGRVKF 175

RESULT 12
Q65RV6_MANSM

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ID Q65RV6_MANSM PRELIMINARY; PRT; 177 AA.
AC Q65RV6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MS1697;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens."
RT succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AB016827; AAU3768.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 177 AA; 18969 MW; B6ACF0AA75915B57 CRC64;

Query Match 35.0%; Score 303.5; DB 2; Length 177;
Best Local Similarity 40.2%; Pred. No. 8.1e-19;
Matches 74; Conservative 25; Mismatches 68; Indels 17; Gaps 6;

Qy 1 MKKALATLI-ALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDL 59
Db 1 MKKTLTALIIAALAMVSAQA----NVYVEGNAGYSKIKSGEVSDFRSPNVALGYDTGDM 56

Qy 60 RPAVDYTRYKNYKAPSTDPFKLYSGASAIYDFDTQSPVKPYLGARLSLNRSASVDL----- 114
Db 57 RYADIDYTHYGKSTDGNSEVKAHGFVSAIYDIEVGSVPKPYIGARLSAN--DIDAKEKR 114

Qy 115 -GGSDSPFSQT---SIGLGLVLTGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSVGV 170
Db 115 SGGSRIRKETDSYKLGALAGVQYQAKVSLNGVVEYNELGKANG-HNINQYGARVGV 173

Qy 171 RVKF 174
Db 174 RYDF 177

RESULT 13
Q65TE2_MANSM
ID Q65TE2_MANSM PRELIMINARY; PRT; 226 AA.
AC Q65TE2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MS1161;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens."
RT succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
DR EMBL; AB016827; AAU3768.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.

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	Query Match	28.5%; Score 247; DB 2; Length 256;
	Best Local Similarity	28.3%; Pred. No. 1.3e-13;
	Matches	69; Conservative 33; Mismatches 64; Indels 78; Gaps 7;
QY	8 LIALALPAALAARGASGFFVQAADAHA-	-KASSSLGS-----AKGFS 47
Dd	: : :   :	:   :   :   :   :   :   :   :
Dd	14 LFSSAAQAASESGHGPFYYVOADLAYAERITHYPKATGANNTSTVSDFRNRRAHSIH	73
QY	48 PRISAGRYINDLRFADVDTTRYK----	--NYKAPSTDFK-----LYS 82
Dd	: : :   :	:   :   :   :   :   :   :   :
Dd	74 PRRSVGVDRFCGWRIAADYASYRKESNSTKKVTEDIADNYSKETKEHQNGSGFHAASS	133
QY	83 IGASAIYDFTDSFPVKPYLGARLSLN--	-----ASVDLGG-----116
Dd	:	:   :   :   :   :   :   :   :
Dd	134 LGLSAIYDFEKLNDKFEPYGICARVAYGHVQHSHSVETKTITTVTSKPATSQGPGPIIQTD	193
QY	117 -----SDSPSQTSGIGLVLTGVSYAIVTPNVDLGDAGRVYNVI GKVNIVKNVRSEL SVG	170
Dd	: : :   :   :   :   :   :   :   :   :	: : :   :   :   :   :   :   :   :   :
Dd	194 PKPPHYHESHSSILGLGIAGVGFDIIPKTLTLDGYRYHNWGRLENTR-FKTHEVSLGM	252
QY	171 RVKVF 174	
Dd	: :	
Dd	253 RYRP 256	
 RESULT 15 Q9CM19_PASMU PRELIMINARY;      PRT;     186 AA.		
ID	Q8CM19_PASMU PRELIMINARY;	PRT;     186 AA.
AC	Q9CM19;	
DC	01-JUN-2001 (TrEMBLrel. 17, Created)	
DD	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DN	Opa.	
GN	Name=opa: OrderedLocusNames=PM1025;	
OS	Pasteurella multocida.	
OC	Bacterii; Proteobacteria; Gammaproteobacteria; Pasteurellales;	
OT	Pasteurellaceae; Pasteurella.	
OX	NCBI_TaxID=747;	
RX	[1]_SEQUENCE.	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=Pm70;	
CC	MEDLINE=21145866; PubMed=11248100; DOI=l0.1073/pnas.051634598;	
LA	May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;	
RA	"Complete genomic sequence of Pasteurella multocida Pm70.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).	
DR	EBEL; ASB06143; AAK03109.1; -; Genomic_DNA.	
DR	HSSP; Q9RPL7; IP4T.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0015288; F:pore activity; IEA.	
DR	InterPro; IPR0003394; Porin_opacity.	
KW	Pfam; PF02462; Opacity; 1.	
SQ	Complete proteome.	
	SEQUENCE 186 AA;       20512 MW;   1B17F0A4ACFC0157 CRC64;	
 Query Match                  28.4% ; Score 246.5 ; DB 2; Length 186; Best Local Similarity      32.3% ; Pred. No. 9.6e-14; Matches   61; Conservative   32; Mismatches   77; Indels   19; Gaps   5		
QY	1 MKKAALTIALLAAPAAAEAGSGTFVVQDAAHAK---	ASSSLGSAGKGFSPRISAGRIN 57
Dd	: : :   :	:   :   :   :   :   :   :   :
Dd	2 MKK---SLLVAIGA LCSLTASANFYQQDGVLGAVTKFSSYSEMNKTNI PVNSVGV DLG	58
QY	58 DIRFAVDYTTRYKNKYAPS-----	TDPKLYSIGASAIYDPTQSVPKPYLCARLSLN 108
Dd	: : :   :	:   :   :   :   :   :   :   :
Dd	59 AMRLDALDYTHYKGFGTSYFGVNOKEHVSYTYGLGLSAFYDENINSVL KPVGM RLASN	118
QY	109 RASVDLGGSDSF---	SQT SIGLGLVALTGVS YAVTP NVDDL D AGRYNYIK VNIV KN VRSGE 165
Dd	: : :   :	:   :   :   :   :   :   :   :
Dd	119 IFDIENKSNFRFESEKTKLYGYFIAGAQLMTNL FVNGIEY NLRGR FS DT-SVNQYG	177
QY	166 LSVMKVNF 174	
Dd	: :	
Dd	178 AKVGLFYDF 186	
Dd	: :	

Search completed: January 11, 2006, 15:21:28  
Job time : 163 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 11, 2006, 15:16:52 ; Search time 45 Seconds  
(without alignments)  
319.679 Million cell updates/sec

Title: US-10-650-123-2  
Perfect score: 868  
Sequence: 1 MKKALATLIALPALALAE.....VNTVKNVRSGELSGVGRVKF 174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/PCUTUS COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	2	US-08-913-362-2
2	854	98.4	174	2	US-08-913-362-6
3	838.5	96.6	175	2	US-08-913-362-30
4	825	95.0	174	2	US-08-913-362-8
5	824.5	95.0	175	2	US-08-913-362-4
6	135	15.6	170	1	US-08-127-499A-20
7	135	15.6	170	1	US-08-482-847-20
8	133	15.3	25	2	US-08-913-362-26
9	113.5	13.1	98	2	US-09-540-236-2245
10	109.5	12.6	187	2	US-09-489-039A-13659
11	104.5	12.0	384	2	US-09-543-681A-7922
12	93	10.7	190	2	US-09-543-681A-7684
13	92.5	10.7	261	2	US-09-252-991A-19759
14	89.5	10.3	186	2	US-09-540-236-2792
15	89.5	10.3	385	2	US-09-489-039A-7451
16	88.5	10.2	186	2	US-09-164-714-7
17	88.5	10.2	573	2	US-09-336-447A-3
18	88.5	10.2	573	2	US-09-952-267B-3
19	88	10.1	359	1	US-08-457-997B-2
20	88	10.1	359	2	US-08-467-722A-2
21	88	10.1	359	2	US-09-451-184-2
22	88	10.1	397	2	US-09-902-540-16267
23	88	10.1	610	2	US-09-336-447A-11
24	88	10.1	610	2	US-09-952-267B-11
25	88	10.1	624	2	US-09-336-447A-7
26	88	10.1	624	2	US-09-952-267B-7
27	88	10.1	889	2	US-09-336-447A-15

28	88	10.1	889	2	US-09-952-267B-15
29	87.5	10.1	708	2	US-09-336-115C-2
30	87	10.0	16	2	US-08-913-362-15
31	87	10.0	500	2	US-09-325-932A-149
32	86	9.9	512	2	US-09-059-584-57
33	85.5	9.9	238	2	US-09-902-540-12284
34	85.5	9.9	487	2	US-09-328-352-5331
35	85	9.8	568	4	PCT-US95-13749-5
36	84.5	9.7	643	2	US-09-328-352-5146
37	84	9.7	351	2	US-09-252-991A-30094
38	83.5	9.6	721	2	US-09-328-352-7781
39	83	9.6	364	2	US-09-418-980-8
40	83	9.6	364	2	US-09-809-665A-151
41	83	9.6	364	2	US-09-506-078-45
42	82	9.4	172	2	US-09-902-540-14682
43	82	9.4	433	1	US-08-883-515-2
44	82	9.4	433	2	US-09-770-509-27
45	82	9.4	512	2	US-09-059-584-56

ALIGNMENTS

RESULT 1  
US-08-913-362-2  
; Sequence 2, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913.362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406.362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001.983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-913-362-2

Query Match 100.0% Score 868; DB 2; Length 174;

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Best Local Similarity 100.0%; Pred. No. 5.9e-93;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174
Db 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174

Qy 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174
Db 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174

RESULT 2
US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; FILING DATE: 17-MAR-1995
; NAME: Bent, Stephen A.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-6

Query Match 98.4%; Score 854; DB 2; Length 174;
Best Local Similarity 98.3%; Pred. No. 2.5e-91;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174
Db 121 SQTSGIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174

RESULT 3
US-08-913-362-30
; Sequence 30, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.362
; FILING DATE: 17-MAR-1995
; FILING DATE: 17-MAR-1995
; NAME: Bent, Stephen A.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-30

Query Match 96.6%; Score 838.5; DB 2; Length 175;
Best Local Similarity 97.1%; Pred. No. 1.6e-89;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDS 119
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRRASVDLGGSDS 120

Qy 120 PSQTSIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174
Db 120 PSQTSIGLVLTGVSAYATPNVDLDAGYRNYIGKVTNTKNNRSGELSVGVRVKF 174
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Db 121 FSQTSXGLGLVAGSVYAVTPNVLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

## RESULT 4

US-08-913-362-8

; Sequence 8, Application US/08913362

; Patent No. 6287574

; GENERAL INFORMATION:

; APPLICANT: Brodeur, Bernard R

; APPLICANT: Martin, Denis

; APPLICANT: Hamel, Josee

; APPLICANT: Rioux, Clement

; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/913,362

; FILING DATE: 13-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/406,362

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/001,983

; FILING DATE: 04-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 047998/0128

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 174 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-913-362-8

Query Match 95.0%; Score 825; DB 2; Length 174;

Best Local Similarity 94.3%; Pred. No. 6.1e-88;

Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALALIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120

Qy 121 SQTSLGLVLTGVSAYVTPNVLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 SKTSAGLGLVAGSVYAVTPNVLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

## RESULT 5

US-08-913-362-4

; Sequence 4, Application US/08913362

; Patent No. 6287574

; GENERAL INFORMATION:

; APPLICANT: Brodeur, Bernard R

; APPLICANT: Martin, Denis

; APPLICANT: Hamel, Josee

; APPLICANT: Rioux, Clement

; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/913,362

; FILING DATE: 13-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/406,362

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/001,983

; FILING DATE: 04-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 047998/0128

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 175 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-913-362-4

Query Match 95.0%; Score 824.5; DB 2; Length 175;

Best Local Similarity 95.4%; Pred. No. 7e-88;

Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALALIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 119

Db 61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 120

Qy 120 FSQTSIGLVLTVGSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 FSQTSIGLVLTVGSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

## RESULT 6

US-08-127-499A-20

; Sequence 20, Application US/08127499A

; Patent No. 5510264

; GENERAL INFORMATION:

; APPLICANT: VAN ALSTYNE, Diane

; APPLICANT: SHARMA, Lawrence Rajendra

; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED

; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127.499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-20

Query Match 15.6%; Score 135; DB 1; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.4e-07;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

Qy 6 ATLIALPALAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
Db 15 SSLFSSAAQAASEDRSPYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAH 74
Qy 46 FSPRISAGYRINDLRPAVDYTRYKNY-----KAPSTDFFK 79
Db 75 IHPRVSGYDGGWRIADYASYRKNWNNKYSVNTKELENKHNKKDKLTENQENGTFHA 134
Qy 80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
Db 135 ASSLGSAIYDFKLGKFKPYIGARVAYGHVRHSID 170

RESULT 7
US-08-482-847-20
; Sequence 20, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.847
; FILING DATE: 07-JUN-1995

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-482-847-20

Query Match 15.6%; Score 135; DB 1; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.4e-07;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

Qy 6 ATLIALPALAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
Db 15 SSLFSSAAQAASEDRSPYVQADLAYAAERITHDYPQATGANNTSTVSDYFRNIRAH 74
Qy 46 FSPRISAGYRINDLRPAVDYTRYKNY-----KAPSTDFFK 79
Db 75 IHPRVSGYDGGWRIADYASYRKNWNNKYSVNTKELENKHNKKDKLTENQENGTFHA 134
Qy 80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
Db 135 ASSLGSAIYDFKLGKFKPYIGARVAYGHVRHSID 170

RESULT 8
US-08-913-362-26
; Sequence 26, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913.362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768

```

REFERENCE/DOCKET NUMBER: 047998/0128  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Neisseria meningitidis  
STRAIN: 608B  
US-08-913-362-26

Query Match 15.3%; Score 133; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 FADVTRYKNYKAPSTDFKLYSIGA 85  
Db 1 FADVTRYKNYKAPSTDFKLYSIGA 25

RESULT 9  
US-09-540-236-2245  
Sequence 2245, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2005-001  
CURRENT APPLICATION NUMBER: US/09/540,236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 2245  
LENGTH: 98  
TYPE: PRT  
ORGANISM: M.catarrhalis  
US-09-540-236-2245

Query Match 13.1%; Score 113.5; DB 2; Length 98;  
Best Local Similarity 37.9%; Pred. No. 1.9e-05;  
Matches 22; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

Qy 122 QTSIGLVLTGVSVAVTNVDLAGRYNYIG---KNTVKNVRSGB--LSGVGVKVF 174  
Db 41 ETKVGFVLAGAQAIVNPQLSDAGVEYNILGKYLKLDTSKLAHQYCAKVGRLHNF 98

RESULT 10  
US-09-489-039A-13699  
Sequence 13699, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 13699  
LENGTH: 187  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13699

Query Match 12.6%; Score 109.5; DB 2; Length 187;

Best Local Similarity 25.2%; Pred. No. 0.00015;  
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Db 107 GGGAELPLGQ-YFTLFGEGYSPDSMSSGVEDYVEANAGVRLNVRPSLNIEAGYRIIDMA 165  
Qy 153 GKVTNVTKNVRSGLSVGVKVF 174  
Db 166 GRDGNEDNTLADGAYAGVNF 187

RESULT 11  
US-09-543-681A-7922  
Sequence 7922, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 7922  
LENGTH: 384  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-7922

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Best Local Similarity 26.1%; Pred. No. 0.0017;  
Matches 55; Conservative 27; Mismatches 86; Indels 43; Gaps 13;

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Qy 47 SPRIS----AGYRIND---LRPAVDYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97  
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RESULT 12  
US-09-543-681A-7684  
Sequence 7684, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706





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Job time : 46 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 19:49:08 ; Search time 3313 Seconds  
(without alignments)  
9007.791 Million cell updates/sec

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Perfect score: 525  
Sequence: 1 atgaaaaagcactgtccac.....gcgtgcgcgtcaattctga 525

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pa.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_ats.\*
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- 12: gb\_un.\*
- 13: gb\_vl.\*
- 14: gb\_hgt.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	525	100.0	525	1	AF175682 Neisseria
3	525	100.0	525	1	AF175683 Neisseria
4	525	100.0	525	6	CQ786532 Sequence
5	525	100.0	525	6	CQ814512 Sequence
6	525	100.0	830	1	U52066 Neisseria m
7	525	100.0	830	6	AF167414 Sequence
8	521.8	99.4	525	1	AF175678 Neisseria
9	521.8	98.4	110000	1	Continuation (7 of
10	521.8	99.4	349980	6	AX044030 Sequence
11	518.6	98.8	850	1	U52068 Neisseria m
12	518.6	98.8	850	6	AF167416 Sequence
13	518.6	98.8	311321	1	NMA322491 Neisseria
14	517	98.5	525	1	AF175677 Neisseria
15	517	98.5	525	1	AF175679 Neisseria
16	515.4	98.2	525	1	AF175676 Neisseria
17	515.4	98.2	525	1	AF175681 Neisseria
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## ALIGNMENTS

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LOCUS AF175680 525 bp DNA linear BCT 06-SEP-1999  
DEFINITION Neisseria meningitidis strain M986 surface protein A (nsrA) gene,  
complete cds.  
ACCESSION AF175680  
VERSION AF175680.1 GI:5825535  
KEYWORDS  
SOURCE Neisseria meningitidis  
ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseria

REFERENCE 1 (bases 1 to 525)  
AUTHORS Moe, G.R., Tan, S. and Granoff, D.M.  
TITLE Differences in Surface Expression of Neisserial Surface Protein A  
among Neisseria meningitidis Group B strains  
JOURNAL Infect Immun. (1999) in press  
REFERENCE 2 (bases 1 to 525)  
AUTHORS Moe, G.R., Tan, S. and Granoff, D.M.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-1999) Children's Hospital Oakland Research  
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

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AF175682	AF175683
LOCUS	LOCUS
DEFINITION	DEFINITION
Neisseria meningitidis strain NG6/88 surface protein A (nspA) gene, complete cds.	Neisseria meningitidis strain NGP165 surface protein A (nspA) gene, complete cds.
ACCESSION	ACCESSION
AF175682	AF175683
VERSION	VERSION
AF175682.1	AF175683.1
KEYWORDS	KEYWORDS
GI:5825540	GI:5825542
SOURCE	SOURCE
Neisseria meningitidis	Neisseria meningitidis
ORGANISM	ORGANISM
Neisseria meningitidis	Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.	Neisseriaceae; Neisseria.
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Moe,G.R., Tan,S. and Granoff,D.M.	Moe,G.R., Tan,S. and Granoff,D.M.
Differences in Surface Expression of Neisserial Surface Protein A	Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains	among Neisseria meningitidis Group B strains
Infect. Immun. (1999) In press	Infect. Immun. (1999) In press
2 (bases 1 to 525)	2 (bases 1 to 525)
Moe,G.R., Tan,S. and Granoff,D.M.	Moe,G.R., Tan,S. and Granoff,D.M.
Direct Submission	Direct Submission
Submitted (04-AUG-1999) Children's Hospital Oakland Research	Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA	Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
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TITLE Direct Submission  
JOURNAL Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA  
FEATURES  
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Query Match 100.0%; Score 525; DB 1; Length 525;  
Best Local Similarity 100.0%; Pred. No. 1.2e-89;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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LOCUS CQ786532 525 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 1 from Patent WO2004019976.  
ACCESSION CQ786532  
VERSION CQ786532.1 GI:45721576  
KEYWORDS  
SOURCE Neisseria meningitidis

ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
REFERENCE 1  
AUTHORS Martin, D. and Rioux, S.  
TITLE Pharmaceutical liposomal compositions containing n. Meningitidis  
JOURNAL derived polypeptides or polynucleotides  
Patent: WO 2004019976-A 1 11-MAR-2004;  
SHIRE BIOCHEM, INC. (CA)  
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Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 481 GTCCGTTCCGGCGAATCTGTCGTCGCGCTGCGCGTCAAAATCTGA 525  
Db 481 GTCCGTTCCGGCGAATCTGTCGTCGCGCTGCGCGTCAAAATCTGA 525  
RESULT 5  
LOCUS CQ814512 525 bp DNA linear PAT 24-MAY-2004  
DEFINITION Sequence 8 from Patent WO2004020452.  
ACCESSION CQ814512  
VERSION CQ814512.1 GI:47603711  
KEYWORDS  
SOURCE Neisseria meningitidis  
ORGANISM Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.  
REFERENCE 1  
AUTHORS Biemans, R., Bos, M., Denoel, P., Peron, C., Goraj, K., Poolman, J.,  
Tommaassen, J. and Weynants, V.  
TITLE Refolding method

JOURNAL Patent: WO 2004020452-A 8 11-MAR-2004;  
 GlaxoSmithKline Biologics S.A. (BE); Utrecht University (NL)

FEATURES  
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 Location/Qualifiers  
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 /organism="Neisseria meningitidis"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:487"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 1.1e-89;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGACATTGCCACACTGATTCCTCGCTCTCCGGCGCGCGCACTGGCGGAA 60  
 Db 1 ATGAAAAAGACATTGCCACACTGATTCCTCGCTCTCCGGCGCGCGCACTGGCGGAA 60

Qy 61 GGCGATCCGGCTTTTACGTCAAGCGATGCCGACACGCAAGAAAGCTCAAGCTCTTTA 120  
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Qy 121 GGTTCGCAAGGCTTCAGCGCGGCTTCGGAGGCTACCGCATCAACGACCTCCGC 180  
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Qy 361 AGCCAAACTCCATCGGCTCGGCTATTGACGGCGTAAGCTATGCCGTTACCCGAAAT 420  
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Qy 421 GTCGATTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480  
 Db 421 GTCGATTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480

Qy 481 GTCCGTTCCGCGAACTGTCGTCGGCTGCGGCTCAAAATCTGA 525  
 Db 481 GTCCGTTCCGCGAACTGTCGTCGGCTGCGGCTCAAAATCTGA 525

RESULT 6  
 NMU52066  
 LOCUS  
 DEFINITION Neisseria meningitidis outer membrane protein gene, complete cds.  
 ACCESSION U52066  
 VERSION U52066.1 GI:1518521  
 KEYWORDS  
 SOURCE Neisseria meningitidis  
 ORGANISM Neisseria meningitidis  
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 Neisseriaceae; Neisseria.

REFERENCE  
 AUTHORS Martin,D., Cadieux,N., Hamel,J. and Brodeur,B.R.  
 TITLE Highly conserved Neisseria meningitidis surface protein confers protection against experimental infection  
 J. Exp. Med. 185 (7), 1173-1183 (1997)  
 9104804

REFERENCE  
 AUTHORS 2 (bases 1 to 830)  
 TITLE Antigenic and molecular conservation of the gonococcal NspA protein  
 Infect. Immun. 67 (6), 2855-2861 (1999)  
 10338491

REFERENCE 3 (bases 1 to 830)  
 AUTHORS Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R. and Martin,D.  
 TITLE Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein  
 Infect. Immun. 67 (9), 4955-4959 (1999)

JOURNAL  
 PUBMED 10456958

REFERENCE 4 (bases 1 to 830)  
 AUTHORS Martin,D.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-MAR-1996) Denis Martin, Department of Microbiology, University Laval, Unite de Vaccinologie, Laboratoire et Service d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705 boul Laurier, Ste-Foy, Quebec G1V 4G2, Canada

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 ORIGIN

Query Match 100.0%; Score 525; DB 1; Length 830;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-89;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 203 GGCGCATCCGCTTTTACGTCCAGCGCGATGCCGACACGCAAGAAAGCTCAAGCTCTTTA 262

Qy 121 GGTTCGCCAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180  
 Db 263 GGTTCGCCAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 322

Qy 181 TTGCGCTCGATTAACACGCGCTACAAAATATATAAGCCCATCCACGATTTCAAACTT 240  
 Db 323 TTGCGCTCGATTAACACGCGCTACAAAATATATAAGCCCATCCACGATTTCAAACTT 382

Qy 241 TACAGCATCGCGCTCGGCTTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 300  
 Db 383 TACAGCATCGCGCTCGGCTTTACGACTTCGACACCCCAATCGCCGTCAAAACCGTAT 442

Qy 301 CTGCGCGCGCTTGAGCTCAACGCGGCTTCGCTCGACTTTGGGCGGCGAGCAGCTTC 360  
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QY 481 GTCCGTTCCGGCGAAGTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 525  
Db 623 GTCCGTTCCGGCGAAGTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 667

## RESULT 7

LOCUS AR167414 AR167414 830 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 1 from patent US 6287574.  
ACCESSION AR167414

VERSION AR167414.1 GI:17903193

## KEYWORDS

SOURCE Unknown.

## ORGANISM

Unclassified.

## REFERENCE

1 (bases 1 to 830)  
Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.

TITLE Proteinase K resistant surface-protein of neisseria meningitidis

JOURNAL Patent: US 6287574-A 1 11-SEP-2001

## FEATURES

Location/Qualifiers

1..830

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 525; DB 6; Length 830;  
Best Local Similarity 100.0%; Pred. No. 1.1e-89;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACTGATTCGCTCTCCGGCGCGCGCACTGGCGGAA 60  
Db 143 ATGAAAAAGCACTTGCACACTGATTCGCTCTCCGGCGCGCGCACTGGCGGAA 202

QY 61 GCGCATCCGGCTTTTACGTCAAGCCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 120  
Db 203 GCGCATCCGGCTTTTACGTCAAGCCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 262

QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGCACTTCGCG 180  
Db 263 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGCACTTCGCG 322

QY 181 TTGCGGTCGATTAACGGGTACAAAATATATAAGCCGATCAACCGATTTCAAACTT 240  
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QY 421 GTGCAATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480  
Db 563 GTGCAATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 622

QY 481 GTCCGTTCCGGCGAAGTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 525  
Db 623 GTCCGTTCCGGCGAAGTGTCCGTCGGCGTGGCGTCAAAATTTCTGA 667

## RESULT 8

LOCUS AF175678 AF175678 525 bp DNA linear BCT 06-SEP-1999  
DEFINITION Neisseria meningitidis strain CU385 surface protein A (nspA) gene,  
complete cds.

## ACCESSION

AF175678

VERSION AF175678.1 GI:5825530

## KEYWORDS

## SOURCE

Neisseria meningitidis  
Neisseria meningitidis  
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.

## REFERENCE

## AUTHORS

Moe, G.R., Tan, S. and Granoff, D.M.

TITLE Differences in Surface Expression of Neisserial Surface Protein A

JOURNAL among Neisseria meningitidis Group B strains

REFERENCE Infect. Immun. (1999) In press

## AUTHORS

Moe, G.R., Tan, S. and Granoff, D.M.

## TITLE

Direct Submission

## JOURNAL

Submitted (04-AUG-1999) Children's Hospital Oakland Research

Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

## FEATURES

Location/Qualifiers

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/mol\_type="genomic DNA"

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## CDS

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## ORIGIN

Query Match 99.4%; Score 521.8; DB 1; Length 525;  
Best Local Similarity 99.6%; Pred. No. 4.7e-89;  
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACTGATTCGCTCTCCGGCGCGCGCACTGGCGGAA 60  
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DEFINITION Neisseria meningitidis outer membrane protein gene, complete cds.
ACCESSION  U52068
VERSION     U52068.1  GI:1808966
KEYWORDS   .
SOURCE      Neisseria meningitidis
ORGANISM    Neisseria meningitidis
            Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
            Neisseriaceae; Neisseria.
REFERENCE   1  (bases 1 to 850)
AUTHORS     Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R. and
            Martin,D.
TITLE       Bactericidal and cross-protective activities of a monoclonal
            antibody directed against Neisseria meningitidis NspA outer
            membrane protein
JOURNAL     Infect. Immun. 67 (9), 4955-4959 (1999)
PUBMED      10456958
REFERENCE   2  (bases 1 to 850)
AUTHORS     Martin,D.
TITLE       Direct Submission
JOURNAL     Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,
            University Laval, Unite de Vaccinologie, Laboratoire et Service
            d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
            boul Laurier, Ste-Foy, Quebec G1V 4G2, Canada
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Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db      328  GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 387

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Db      448  TACAGCATCCGGCGCTCCGCCATTTACGATTCGACACCCCAATGCCCGTCAACCGTAT 507

QY      301  CTGGCGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGGCGGCGAGCAGCTTC 360
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QY      361  AGCCAAACCTCCATCGGCTCGGCTATTGACGGCGTAAAGCTATGCGCTTACCCCGAAT 420
Db      568  AGCCAAACCTCCATCGGCTCGGCTATTGACGGCGTAAAGCTATGCGCTTACCCCGAAT 627

QY      421  GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480

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LOCUS NMA3Z2491 311321 bp DNA linear BCT 16-APR-2005  
 DEFINITION Neisseria meningitidis serogroup A strain Z2491 complete genome;  
 segment 3/7.

ACCESSION AL162754 AL157959  
 VERSION AL162754.2 GI:7379424

KEYWORDS

SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS

Neisseria meningitidis Z2491  
 Neisseria meningitidis Z2491  
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 Neisseriaceae; Neisseria.  
 1 (bases 1 to 311321)  
 Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,  
 Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,  
 Davies,K.M., Davis,P., Devlin,K., Feitwell,T., Hamlin,N.,  
 Holroyd,S., Jagsis,K., Leather,S., Moule,S., Mungall,K.,  
 Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,  
 Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.  
 Complete DNA sequence of a serogroup A strain of Neisseria  
 meningitidis Z2491  
 Nature 404 (6777), 502-506 (2000)  
 10761919  
 2 (bases 1 to 311321)  
 Parkhill,J.

Direct Submission  
 Submitted (30-MAR-2000) Submitted on behalf of the Neisseria  
 sequencing team, Sanger Centre, Wellcome Trust Genome Campus,  
 Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

TITLE

Notes:  
 Details of N. meningitidis sequencing at the Sanger Centre are  
 available on the World Wide Web.  
 (URL, [http://www.sanger.ac.uk/Projects/N\\_meningitidis/](http://www.sanger.ac.uk/Projects/N_meningitidis/)).

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CDS

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fasta scores; E(): 5.1e-32, 58.0% identity in 138 aa
overlap. Shows very weak similarity to eukaryotic
6-pyruvoyl-tetrahydropterin synthases e.g. SW:PTPS_RAT

Query Match 98.8%; Score 518.6; DB 1; Length 311321;
Best Local Similarity 99.2%; Pred. No. 1.1e-88;
Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 14
AF175677 525 bp DNA linear BCT 06-SEP-1999
LOCUS AF175677
DEFINITION Neisseria meningitidis strain BZ232 surface protein A (nsaP) gene,
complete cds.
ACCESSION AF175677
VERSION AF175677.1 GI:5825528
KEYWORDS Neisseria meningitidis
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 525)
Moe, G.R., Tan, S. and Granoff, D.M.
Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains
Infect. Immun. (1999) In press
JOURNAL REFERENCE 2 (bases 1 to 525)
Moe, G.R., Tan, S. and Granoff, D.M.
Direct Submission
AUTHORS Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
JOURNAL Location/Qualifiers
FEATURES
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Query Match		98.5%; Score 517; DB 1; Length 525;		Best Local Similarity		99.0%; Pred. No. 3.8e-88;	
Matches		520; Conservative		0; Mismatches		5; Indels	
0;				0; Gaps		0;	
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Qy	61	GGCGCATCCGGCTTTTACGTCAAGCCGATCCCGGACACGCAAAAGCCTCAAGCTCTTTA	120	Qy	61	GGCGCATCCGGCTTTTACGTCAAGCCGATCCCGGACACGCAAAAGCCTCAAGCTCTTTA	120
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Qy	421	GTGCAATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC	480	Qy	421	GTGCAATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC	480
Db	421	GTGCAATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC	480	Db	421	GTGCAATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC	480
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Job time : 3318 secs

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Query Match		98.5%; Score 517; DB 1; Length 525;		Best Local Similarity		99.0%; Pred. No. 3.8e-88;	
Matches		520; Conservative		0; Mismatches		5; Indels	
0;				0; Gaps		0;	
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Qy	181	TTGCGCGTCGATTAACGCGCTACAAAACTATATAAGCCCATCCACCGATTTCAAACTT	240	Qy	181	TTGCGCGTCGATTAACGCGCTACAAAACTATATAAGCCCATCCACCGATTTCAAACTT	240
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Qy	301	CTCGCGCGCGCTTTGAGCCTCAACCGCGCTTCGACACCCCAATCGCCGTCAAAACCGTAT	360	Qy	301	CTCGCGCGCGCTTTGAGCCTCAACCGCGCTTCGACACCCCAATCGCCGTCAAAACCGTAT	360
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Qy	481	GTCCGTTCCGGCGAACTGTCCGCGGCTGCGCGTCAAAATTTCTGA	525	Qy	481	GTCCGTTCCGGCGAACTGTCCGCGGCTGCGCGTCAAAATTTCTGA	525
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RESULT 15

AP175679

LOCUS

Neisseria meningitidis strain M136 surface protein A (nspA) gene, complete cds.

DEFINITION

AP175679

VERSION

AP175679.1 GI:5825533

KEYWORDS

Neisseria meningitidis

SOURCE

Neisseria meningitidis

ORGANISM

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 525)

Moe,G.R., Tan,S. and Granoff,D.M.

AUTHORS

Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains

JOURNAL

Infect. Immun. (1999) In press

REFERENCE

2 (bases 1 to 525)

Moe,G.R., Tan,S. and Granoff,D.M.

AUTHORS

Direct Submission

TITLE

Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

JOURNAL

Location/Qualifiers

FEATURES

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY\_NUC  
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Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Listing first 45 summaries

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- 3: geneseqn2000s.\*
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- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
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- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	525	100.0	525	12 ADL13427	Adl13427 Neisseria
2	525	100.0	525	12 ADL24351	Adl24351 N meningi
3	525	100.0	830	2 AAT39039	Aat39039 Proteinas
4	525	100.0	830	8 ACA64711	Ac64711 N. mening
5	525	100.0	830	10 ADF43315	Adf43315 N. mening
6	525	100.0	830	14 AEA03009	Aea03009 Neisseria
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8	521.8	99.4	110000	3 AAA81490_06	Continuation (7 of
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10	518.6	98.8	850	2 AAT39041	Aat39041 Proteinas
11	502.6	95.7	710	6 ABS67381	Ab67381 Neisseria
12	502.6	95.7	810	2 AAT39042	Aat39042 Proteinas
13	491.2	93.6	710	2 AAT39040	Aat39040 Proteinas
14	480.2	91.5	525	10 ABZ38961	Abz38961 N. gonorr
15	464.8	88.5	468	12 ADL13425	Adl13425 Neisseria
16	368	70.1	486	10 ABZ38960	Abz38960 N. gonorr
17	63	12.0	75	12 ADJ83984	Adj83984 Neisseria
18	51.4	9.8	985	6 ABQ44816	Abq44816 Oligonuc
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22	49	9.3	13631	4 ABL20354	Abi20354 Drosophil
23	48.6	9.3	1682	12 ADJ39303	Adj39303 Plant cdn
24	47	9.0	1842	8 ADA71243	Ada71243 Rice gene
25	46.8	8.9	72	11 ADM40964	Adm40964 Neisseria
26	46.4	8.8	1329	8 ADA69820	Ada69820 Rice gene
27	46.2	8.8	2346	11 ACL28066	ACL28066 Rice abio
28	45.8	8.7	1282	13 ADT18790	Adt18790 Plant cdn
29	45.6	8.7	1005	2 AAZ30006	Aaz30006 Optimised
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31	45.6	8.7	2607	4 ABL16369	Abi16369 Drosophil
32	45.6	8.7	2781	14 AEB47202	Aeb47202 Chimpanze
33	45.6	8.7	4617	14 AEB91820	Aeb91820 DNA encod
34	45.6	8.7	110000	4 RAI99682_37	Continuation (38 o
35	45.6	8.7	110000	4 RAI99683_37	Continuation (38 o
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37	45.2	8.6	1638	13 ADX64338	Adx64338 Plant ful
38	45	8.6	45	12 ADL24367	Adl24367 N meningi
39	45	8.6	609	9 ACL14692	ACL14692 DNA clone
40	45	8.6	3324	8 ACA38418	Aca38418 Prokaryot
41	45	8.6	9903	8 ACA40315	Aca40315 Prokaryot
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ALIGNMENTS

RESULT 1

ID	ADL13427	standard; DNA; 525 BP.
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AC	ADL13427;	
XX	03-JUN-2004	(first entry)
XX	Neisseria meningitidis H44/76	NspA gene.
DE	Neisseria meningitidis H44/76	NspA gene.
KW	Neisserial surface protein A; NspA; refolding; recombinant production;	
KW	vaccine; subunit vaccine; prevention; diagnosis; meningococcus;	
KW	invasive bacterial disease; bacteraemia; meningitis;	
KW	Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;	
KW	antibacterial; gene therapy; gene; da.	
XX	Neisseria meningitidis; H44/76.	
OS	Neisseria meningitidis; H44/76.	
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WO2004020452-A2.

11-MAR-2004.

28-AUG-2003; 2003WO-EP010085.

30-AUG-2002; 2002GB-00020197.

(GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.  
(UUT-) RIJKSUNIV UTRECHT.

Biemans R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;  
Tommaesen J, Weynants V;

DR WPI; 2004-239150/22.  
 XX P-PSDB; ADL13428.  
 PT New refolded NspA protein, useful for preparing a composition for  
 PT diagnosing, treating or preventing infection caused by *Neisseria*  
 PT meningitidis or *Neisseria gonorrhoeae*.  
 XX  
 XX Disclosure; Fig 3; 62pp; English.  
 XX  
 XX The invention relates to an isolated refolded *Neisseria* surface protein  
 CC A (NspA) from *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The  
 CC invention also relates to the method of refolding an NspA protein; an  
 CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-  
 CC dimethyldecylammoniohexanesulphonate) for refolding an NspA protein; a  
 CC pharmaceutical composition comprising the refolded NspA protein, a  
 CC carrier and optionally one or more other *Neisseria* antigens; a method of  
 CC preventing or treating a *Neisseria* infection; an antibody immunospecific  
 CC for the NspA protein; and diagnosing a *Neisseria* infection. NspA has  
 CC characteristics which indicate that it is a potential vaccine candidate  
 CC for the development of subunit vaccines for the treatment of infections  
 CC caused by *Neisseria meningitidis* (meningococcus), which causes invasive  
 CC bacterial diseases such as bacteraemia and meningitis, or *Neisseria*  
 CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced  
 CC NspA could therefore be used to produce vaccine compositions and it could  
 CC also be used in the development of new antimicrobial agents, diagnostic  
 CC tests and in drug screening. However, recombinantly produced proteins are  
 CC frequently unable to adopt their biologically active conformations, and  
 CC yields may be very low due to mis-folding and aggregation of the protein.  
 CC The method of the invention provides an improved method for refolding the  
 CC NspA protein, and it is possible to increase the recovery of active  
 CC protein form partly purified inclusion bodies in amounts up to 100%  
 CC without the need for further purification. The refolded NspA protein is  
 CC useful for preparing a composition for diagnosing, treating or preventing  
 CC infection caused by *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The  
 CC present sequence represents the NspA gene from *Neisseria meningitidis*  
 CC H44/76.

Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 12; Length 525;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAAAAAGACACTTGCCACACTGATGCGCTCTCCGCGCGCGCACTCGCGGAA 60  
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 QY 481 GTCGATTTGGATGCGCGCTACCGCTACAACTACATTCGCGAAAGTCAACACTGTCTTTA 525  
 DB 481 GTCGATTTGGATGCGCGCTACCGCTACAACTACATTCGCGAAAGTCAACACTGTCTTTA 525  
 RESULT 2  
 ADL24351  
 ID ADL24351 standard; DNA; 525 BP.  
 XX  
 AC ADL24351;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE N meningitidis strain 608B NspA coding sequence.  
 XX  
 KW ds; gene; NspA; vaccine; antibacterial; meningitis.  
 XX  
 OS *Neisseria meningitidis*.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..525  
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 XX  
 PW WC2004019976-A2.  
 XX  
 DD 11-MAR-2004.  
 XX  
 PF 29-APR-2003; 2003WO-CA001452.  
 XX  
 PR 30-AUG-2002; 2002US-0406980P.  
 XX  
 PA (SHIR-) SHIRE BIOCHEM INC.  
 XX  
 PI Martin D, Rioux S;  
 XX  
 WPI; 2004-239123/22.  
 P-PSDB; ADL24352.

Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from *Neisseria meningitidis* strain 608B, or its fragment or analog, useful for inducing an immune response against N. meningitidis.  
 Claim 9; Fig 1; 79pp; English.  
 The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from *Neisseria meningitidis* strain 608B, where the polypeptide is the NspA protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or preventing *Neisseria* infection chosen from N. meningitidis, N. gonorrhoeae, N. lactamica and N. polysacchara. It is useful for treatment or prophylaxis of meningitis and meningococemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is the *Neisseria meningitidis* strain 608B NspA coding sequence.  
 Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 525; DB 12; Length 525;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAAAAAGACACTTGCCACACTGATGCGCTCTCCGCGCGCGCACTCGCGGAA 60  
 DB 1 ATGAAAAAGACACTTGCCACACTGATGCGCTCTCCGCGCGCGCACTCGCGGAA 60  
 QY 61 GGCGCATCCGCGCTTTTACGTCACAGCGGATGCGCGGATGCGCGATCCGATCCGCTCCG 120  
 DB 61 GGCGCATCCGCGCTTTTACGTCACAGCGGATGCGCGGATGCGCGATCCGATCCGCTCCG 120



121	GGTTCTGCCAAGGCTT	CAGCCGCGGCAATCTCCGGAGGCTACCGCATCAACGACCTCCGC	180
121	GGTTCTGCCAAGGCTT	CAGCCGCGGCAATCTCCGGAGGCTACCGCATCAACGACCTCCGC	180
181	TTCCGGCGTCGATTACA	CGCGGCTACAAAACATATAAGCCCNCCACCGGATTTCAAACTT	240
181	TTCCGGCGTCGATTACA	CGCGGCTACAAAACATATAAGCCCNCCACCGGATTTCAAACTT	240
241	TACAGCATCGCGCGCT	CGGCCATTTTACGACTTTCGACACCCAAATCGCCCGCTCAAAACCGTAT	300
241	TACAGCATCGCGCGCT	CGGCCATTTTACGACTTTCGACACCCAAATCGCCCGCTCAAAACCGTAT	300
301	CTCGCGCGCGGCTTGAG	CGCTGAAACCGCGCCTCCGTTCGACTTTGGCGCGCAGCGACAGCTTC	360
301	CTCGCGCGCGGCTTGAG	CGCTGAAACCGCGCCTCCGTTCGACTTTGGCGCGCAGCGACAGCTTC	360
361	AGCAAAACCTCCATCGG	CTCGGGCTATTGACGGCGTAAAGCTATGCGTTACCCCGAAT	420
361	AGCAAAACCTCCATCGG	CTCGGGCTATTGACGGCGTAAAGCTATGCGTTACCCCGAAT	420
421	GTCCGATTTTGGATGCG	CGGCTACCGCTACAACTACATCGGCCAAAGTCAACACTGTCAAAAAC	480
421	GTCCGATTTTGGATGCG	CGGCTACCGCTACAACTACATCGGCCAAAGTCAACACTGTCAAAAAC	480
481	GTCCGTTCCGGCGAACT	GTCCGTGCGGCGTCCAAATTTCTGA	525
481	GTCCGTTCCGGCGAACT	GTCCGTGCGGCGTCCAAATTTCTGA	525

RESULT 3	
AAT39039	
ID	AAT39039 standard; DNA; 830 BP.
XX	
AC	
AAT39039;	
XX	
DT	16-OCT-2003 (revised)
DT	22-DEC-1996 (first entry)

DE Proteinase K resistant *N. meningitidis* 22 kD surface protein.  
XX  
KW Proteinase K resistant; *Neisseria meningitidis*; *Neisseria gonorrhoeae*;  
KW antibody; detection; probe; surface protein; ss.

Key	Location/Qualifiers
key -10_signal	75..80
FT	/*tag= d
FT	
FT	131..135
FT	
RBS	131..135
FT	/*tag= e
FT	
FT	143..667
FT	
CDS	143..667
FT	/*tag= a
FT	
FT	143..199
FT	/*tag= b
FT	
sig_peptide	143..199
FT	/*tag= b
FT	
mat_peptide	200..664
FT	/*tag= c
FT	
FT	

XX\*  
PN WO9629412-A1  
XX  
PD 26-SEP-1996.

XX	15-MAR-1996;	96WO-CA000157.
PF		
XX	17-MAR-1995;	95US-00406362.
PR		
PR	04-AUG-1995;	95US-0001983P.

PA (IAFB-) IAF BIO VAC INC.

PI Brodeur BR, Martin D, Hamel J, Rioux C;

WPI; 1996-443187/44.  
P-PSDB; AAW04891.

[illegible]

*Neisseria meningitidis* antigen, highly conserved strains - useful for prodn. of antibodies for imm diagnosis of, *N. meningitidis* infection.

Claim 12; Fig 1; 117pp; English.

A proteinase K resistant surface protein has been of *N. meningitidis* (AAT39039 to AAT39042). The 1 antigenic fragments of antibodies can be used in prevention of infection by *N. meningitidis* or by humans. The antibodies may also be used diagnostically for *N. meningitidis* infection. The antigen may also be used to detect specific to *N. meningitidis* antigen. DNA sequences encoding or their fragments, can be used as probes for the detection of *Neisseria* bacteria. (Updated on 16-OCT-2003 to standardise *Neisseria* bacteria.

Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 2; Length 830;  
Best Local Similarity 100.0%; Pred. No. 5.9e-125;  
Matches 525; Conservative 0; Mismatches 0; Indels 0

1	ATGAAAAAGACATTGCGCACACTGATTGCTTCGCCCTCGCTCTCCGCGCGCGCACTGGCGGAA	60
143	ATGAAAAAGACATTGCCACACTGATTGCTTCGCCCTCGCTCTCCGCGCGCGCACTGGCGGAA	202
61	GGCGCATCCGGCTTTTACGTCCAAGCCGATGCGGCACGACAAAAGCCTCAAGCTCTTTTA	120
203	GGCGCATCCGGCTTTTACGTCCAAGCCGATGCGGCACGACAAAAGCCTCAAGCTCTTTTA	262
121	GGTTCTGCGCAAGGCTTCAGCCGCGCATCTCCGCAAGGCTACCGCATCAACGACCTCCGC	180
263	GGTTCTGCGCAAGGCTTCAGCCGCGCATCTCCGCAAGGCTACCGCATCAACGACCTCCGC	322
181	TTGCGCGTTCGATTACACGCGCTACAAAATCTATAAAGCCCCATCCACCGATTTCAAACTT	240
323	TTGCGCGTTCGATTACACGCGCTACAAAATCTATAAAGCCCCATCCACCGATTTCAAACTT	382
241	TACAGCATCGGCGCGTCGCGCATTTACGACTTCGACACCCCATCGCCCGCTCAACACCGTAT	300
383	TACAGCATCGGCGCGTCGCGCATTTACGACTTCGACACCCCATCGCCCGCTCAACACCGTAT	442
301	CTCGGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGCGCGCACGCA CAGCTTC	360
443	CTCGGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGCGCGCACGCA CAGCTTC	502
361	AGCCAAACTCCATCGGCGCTCGCGTATTGACGGGGGTAAAGCTATGCGCGTTACCCCGAAT	420
503	AGCCAAACTCCATCGGCGCTCGCGGTATTGACGGGGGTAAAGCTATGCGCGTTACCCCGAAT	562
421	GTGCAATTGGAATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC	480
563	GTGCAATTGGAATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC	622
481	GTCCGTTCCGGCGAACTGTCGTCGCGGTGCGGTCAAAATTTCTGA	525
623	GTCCGTTCCGGCGAACTGTCGTCGCGGTGCGGTCAAAATTTCTGA	667

RESULT 4  
ACA64711  
ID ACA64711 standard; DNA; 830 BP.

AC ACA64711;

XX  
DT 18-JUN-2003 (first entry)DE *N. meningitidis* lipopolysaccharide gene.

KW Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer;  
KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;  
KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;  
KW

5462  
+ 2221  
2221



KW tumouricidal immunocyte; antitumour.

XX Neisseria meningitidis.

XX US2002177551-A1.

XX 28-NOV-2002.

XX 30-MAY-2001; 2001US-00870759.

XX 31-MAY-2000; 2000US-0208128P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-361759/34.

XX P-PSDB; ABU79079.

XX A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces energy or apoptosis in T cells and antigen presenting cells.

XX Disclosure; Page; 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumor associated lipids and induces energy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumor associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumor associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumor associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumor associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidal immunocyte population ex vivo in a mammal) by allowing a tumour associated lipid to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumor associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host, treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumor associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated lipid to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumor associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence encodes an anti-tumour protein which is co-administered with or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent

CC office website at "seqdata.uspto.gov/sequence.html?DocID=2002177551"

XX Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 525; DB 8; Length 830;

XX Best Local Similarity 100.0%; Pred. No. 5.9e-125;

XX Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCATTGGCACAATGATGCGCTCTCCGCGCGCGCGCACTCGCGGAA 60

DB 143 ATGAAAAAGCATTGGCACAATGATGCGCTCTCCGCGCGCGCGCACTCGCGGAA 202

QY 61 GGCGCATCCGGCTTTTACGTCCAAAGCGGATGCCGACACGCAAAAGCTCAAGCTCTTTA 120

DB 203 GGCGCATCCGGCTTTTACGTCCAAAGCGGATGCCGACACGCAAAAGCTCAAGCTCTTTA 262

QY 121 GGTTCCTGCAAAAGCTTTCAGCGCGCGCATCTCCGCGCGCGCATCCGCGATCAAGCTCTCGC 180

DB 263 GGTTCCTGCAAAAGCTTTCAGCGCGCGCATCTCCGCGCGCGCATCCGCGATCAAGCTCTCGC 322

QY 181 TTGCGCGCTGATACAGCGCTACAAAACCTATAAAGCCCATCCACCGATTTCAAACTT 240

DB 323 TTGCGCGCTGATACAGCGCTACAAAACCTATAAAGCCCATCCACCGATTTCAAACTT 382

QY 241 TACAGCATCCGGCGCTCCGCCATTTACGATTCGACACCAATCCGCCGTCAAACCGTAT 300

DB 383 TACAGCATCCGGCGCTCCGCCATTTACGATTCGACACCAATCCGCCGTCAAACCGTAT 442

QY 301 CTGCGCGCGCTTGAGCCCTCAACCGCGCTCCGTCGACTTGGGCGCGCGAGCAGCTTC 360

DB 443 CTGCGCGCGCTTGAGCCCTCAACCGCGCTCCGTCGACTTGGGCGCGCGAGCAGCTTC 502

QY 361 AGCCAAACCTCCATCCGCGCTCGGCTATTGACGCGCGCTAAGCTATGCGCTTACCCCGAAT 420

DB 503 AGCCAAACCTCCATCCGCGCTCGGCTATTGACGCGCGCTAAGCTATGCGCTTACCCCGAAT 562

QY 421 GTGATTTGGATCCGCGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 480

DB 563 GTGATTTGGATCCGCGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 622

QY 481 GTGATTTGGATCCGCGCTACCGCTACCGCTACCGCTACCGCTCAAAATCTGA 525

DB 623 GTGATTTGGATCCGCGCTACCGCTACCGCTACCGCTACCGCTCAAAATCTGA 667

RESULT 5

ADP43315

ID ADP43315 standard; DNA; 830 BP.

XX AC ADP43315;

XX DT 12-FEB-2004 (first entry)

XX N. meningitidis lipopolysaccharide DNA seq id 35.

DE receptor; lipid-based tumour associated antigen; cytostatic;

KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;

KW infectious disease; lipopolysaccharide; LPS; ds.

OS Neisseria meningitidis.

XX US2003157413-A1.

XX 21-AUG-2003.

XX 28-DEC-2000; 2000US-00751708.

XX 28-DEC-1999; 99US-0173371P.

XX (TERM/) TERMAN D S.

XX Terman DS;

DR WPI; 2003-787326/74.  
XX P-PSDB; ADF43316.  
XX  
PT New receptor in a mammalian cell that inhibits regular activation by  
PT receptors specific for lipid-based tumor associated antigens, useful for  
PT treating a neoplastic disease or tumor, and infectious diseases.  
XX  
XX  
PS Disclosure; SEQ ID NO 35; 151pp; English.

XX The invention describes a receptor in a mammalian cell that inhibits

CC regular activation by receptors specific for lipid-based tumor  
CC associated antigen. The receptor has cytostatic and antimicrobial  
CC properties and is suitable for use in gene therapy. The receptors,  
CC methods and compositions are useful for treating a neoplastic disease or  
CC tumor (cancer), and infectious diseases. This sequence encodes *Neisseria*  
CC meningitidis lipopolysaccharide (LPS) to which tumor cells develop  
CC immunity.

XX SQ Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 10; Length 830;  
Best Local Similarity 100.0%; Pred. No. 5.9e-125;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 60  
Db 143 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 202  
Qy 61 GGCGCATCCGGCTTTTACGTCCAGCGATGCGGCACACGCAAGAGCTCAAGCTCTTTA 120  
Db 203 GGCGCATCCGGCTTTTACGTCCAGCGATGCGGCACACGCAAGAGCTCAAGCTCTTTA 262  
Qy 121 GGTTCGCAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGAGCTCTTTA 180  
Db 263 GGTTCGCAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGAGCTCTTTA 322  
Qy 181 TTGCGCGTTCGATACACGCGCTACAAAATATATAAGCCCATCCAGATTTCAAACTT 240  
Db 323 TTGCGCGTTCGATACACGCGCTACAAAATATATAAGCCCATCCAGATTTCAAACTT 382  
Qy 241 TACAGCATCCGGCTTCGCGCAATTTACGATTCGACACCAATCCCGCTCAAGCTAT 300  
Db 383 TACAGCATCCGGCTTCGCGCAATTTACGATTCGACACCAATCCCGCTCAAGCTAT 442  
Qy 301 CTGCGCGCGCTTCGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGAGCAGCTTC 360  
Db 443 CTGCGCGCGCTTCGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGCGAGCAGCTTC 502  
Qy 361 AGCCAAACCTCCATCGGCTCGGGCTATTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 420  
Db 503 AGCCAAACCTCCATCGGCTCGGGCTATTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 562  
Qy 421 GTCGATTTGGATCCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480  
Db 563 GTCGATTTGGATCCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 622  
Qy 481 GTCCGCTTCGGGCAACTGTCCTCGGCTCGCGCTCAAAATTTCTGA 525  
Db 623 GTCCGCTTCGGGCAACTGTCCTCGGCTCGCGCTCAAAATTTCTGA 667

RESULT 6

AEA03009

ID AEA03009 standard; DNA; 830 BP.

XX AC AEA03009;

XX 28-JUL-2005 (first entry)

DE *Neisseria meningitidis* meningococcal meningitis DNA SEQ ID NO:35.  
XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic; meningitis;  
KW gene; ds.

XX *Neisseria meningitidis*.  
XX OS US2005112141-A1.  
XX PN 26-MAY-2005.  
XX PP 08-SEP-2004; 2004US-00937758.  
XX PR 30-AUG-2000; 2000US-00650884.  
XX (TERM/) TERMAN D S.  
XX Terman DS;  
XX WPI; 2005-394926/40.  
XX P-PSDB; AEA03010.  
XX  
XX New composition for treating a tumor or neoplastic disease in a subject  
XX comprises conjugates comprising superantigen polypeptides or nucleic  
XX acids with other molecules that produce a tumoricidal response.  
XX  
XX Disclosure; SEQ ID NO 35; 125pp; English.

XX The invention relates to a composition for treating a tumor or neoplastic  
XX disease in a subject. Also described: (1) a mammalian cell comprising an  
XX exogenous nucleic acid encoding a superantigen expressed in the cell,  
XX which cell also produces or expresses all alpha-anomers of  
XX monoglycosylceramide or diglycosylceramide, where expression of the  
XX superantigen and the mono- or diglycosylceramide is capable of eliciting  
XX an antitumor immune response in a mammal into which the cell is  
XX introduced; (2) treating a tumor or neoplastic disease in a subject; (3)  
XX preparing a population of immunotherapeutic T or natural killer T (NKT)  
XX cells useful to treat a tumor or neoplastic disease in a subject; (4) an  
XX apoptotic cell preparation or lysate useful for treating a tumor or  
XX neoplastic disease in a subject, comprising a cell population that has  
XX been transfected with naked DNA encoding a superantigen, and treated to  
XX undergo apoptosis or lysis; and (5) a cell that has ingested or been  
XX transfected with the above apoptotic preparation or lysate, thus,  
XX rendering the cell effective in presenting material expressed from  
XX a transfecting nucleic acid or material ingested to the immune system of a  
XX mammal to elicit an anti-tumor immune response. The composition and  
XX methods are useful for treating tumors or neoplastic diseases. The  
XX present sequence represents a *Neisseria meningitidis* nucleotide sequence  
XX which induces meningococcal meningitis, which is given in the  
XX exemplification of the present invention. Note - The sequence data for  
XX this patent is not represented in the printed specification, but was  
XX obtained in electronic format directly from the USPTO web site.

XX SQ Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 14; Length 830;  
Best Local Similarity 100.0%; Pred. No. 5.9e-125;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 60  
Db 143 ATGAAAAAGCACTTGCACACTGATGGCTCTCCGGCCGCGCACTGGCGGAA 202  
Qy 61 GGCGCATCCGGCTTTTACGTCCAGCGATGCGGCACACGCAAGAGCTCTTTA 120  
Db 203 GGCGCATCCGGCTTTTACGTCCAGCGATGCGGCACACGCAAGAGCTCTTTA 262  
Qy 121 GGTTCGCAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGAGCTCTTTA 180  
Db 263 GGTTCGCAAGGCTTCAGCGCGCATCTCCGAGGCTACCGCATCAAGAGCTCTTTA 322  
Qy 181 TTGCGCGTTCGATACACGCGCTACAAAATATATAAGCCCATCCAGATTTCAAACTT 240  
Db 323 TTGCGCGTTCGATACACGCGCTACAAAATATATAAGCCCATCCAGATTTCAAACTT 382  
Qy 241 TACAGCATCCGGCTTCGCGCAATTTACGATTCGACACCAATCCCGCTCAAGCTAT 300

```
Db 383 TACAGCATCGCGCTCGCGCAATTTCAGACTTCGACACACCCAAATCGCCGTCACAAACCGTAT 442
Qy 301 CTCGGCGCGCTTGAGGCTCAACCGGCTCCGTCGACTTGAGCGGCGAGCAGAGCTTC 360
Db 443 CTCGGCGCGCTTGAGGCTCAACCGGCTCCGTCGACTTGAGCGGCGAGCAGAGCTTC 502
Qy 361 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420
Db 503 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 562
Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480
Db 563 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 622
Qy 481 GTCGCTTCGCGCAACTGTCCGTCGGGTCGGCGTCAAAATTCGA 525
Db 623 GTCGCTTCGCGCAACTGTCCGTCGGGTCGGCGTCAAAATTCGA 667

RESULT 7
AAA81490_14/c
Continuation (15 of 15) of AAA81490 from base 1400001 (N. meningitidis B full length gen
WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490
WP Fragment Name Begin End
WP AAA81490_00 1 110000
WP AAA81490_01 100001 210000
WP AAA81490_02 200001 310000
WP AAA81490_03 300001 410000
WP AAA81490_04 400001 510000
WP AAA81490_05 500001 610000
WP AAA81490_06 600001 710000
WP AAA81490_07 700001 810000
WP AAA81490_08 800001 910000
WP AAA81490_09 900001 1010000
WP AAA81490_10 1000001 1110000
WP AAA81490_11 1100001 1210000
WP AAA81490_12 1200001 1310000
WP AAA81490_13 1300001 1410000
WP AAA81490_14 1400001 1437668

Query Match 99.4%; Score 521.8; DB 3; Length 37668;
Best Local Similarity 99.6%; Pred. No. 9.4e-124;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 60
Db 20578 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 20519
Qy 61 GCGCATCCGCGCTTTTACGTCCAGCGCGATGCCGACACGCAAAAGCCTCAAGCTCTTTA 120
Db 20518 GCGCATCCGCGCTTTTACGTCCAGCGCGATGCCGACACGCAAAAGCCTCAAGCTCTTTA 20459
Qy 121 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 180
Db 20458 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 20399
Qy 181 TTCCGCTCGGATTCACGCGCTACAAAATCTATAAGCCCATCAACGATTTCAAACTT 240
Db 20398 TTCCGCTCGGATTCACGCGCTACAAAATCTATAAGCCCATCAACGATTTCAAACTT 20339
Qy 241 TACAGCATCGGCGCTCGCCATTTACGACTTCGACACCCCAATCGCCGTCACAAACCGTAT 300
Db 20338 TACAGCATCGGCGCTCGCCATTTACGACTTCGACACCCCAATCGCCGTCACAAACCGTAT 20279
Qy 301 CTCGGCGCGCTTGAGCTCAACCGGCTCCGTCGACTTGAGCGGCGAGCAGAGCTTC 360
Db 20278 CTCGGCGCGCTTGAGCTCAACCGGCTCCGTCGACTTGAGCGGCGAGCAGAGCTTC 20219
Qy 361 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420
Db 20218 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 20159
Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480
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Db 20158 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 20099
Qy 481 GTCGCTTCGCGCAACTGTCCGTCGGGTCGGGTCGAAATTCGA 525
Db 20098 GTCGCTTCGCGCAACTGTCCGCGGTCGGGTCGAAATTCGA 20054

RESULT 8
AAA81490_06/c
Continuation (7 of 15) of AAA81490 from base 600001 (N. meningitidis B full length genom
WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490
WP Fragment Name Begin End
WP AAA81490_00 1 110000
WP AAA81490_01 100001 210000
WP AAA81490_02 200001 310000
WP AAA81490_03 300001 410000
WP AAA81490_04 400001 510000
WP AAA81490_05 500001 610000
WP AAA81490_06 600001 710000
WP AAA81490_07 700001 810000
WP AAA81490_08 800001 910000
WP AAA81490_09 900001 1010000
WP AAA81490_10 1000001 1110000
WP AAA81490_11 1100001 1210000
WP AAA81490_12 1200001 1310000
WP AAA81490_13 1300001 1410000
WP AAA81490_14 1400001 1437668

Query Match 99.4%; Score 521.8; DB 3; Length 110000;
Best Local Similarity 99.6%; Pred. No. 1.2e-123;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 60
Db 90785 ATGAAAAAGCATTGCCACACTGATTCGCCCTCGCTCTCCGCGCGCGCACTCGCGGAA 90726
Qy 61 GCGCATCCGCGCTTTTACGTCCAGCGCGATGCCGACACGCAAAAGCCTCAAGCTCTTTA 120
Db 90725 GCGCATCCGCGCTTTTACGTCCAGCGCGATGCCGACACGCAAAAGCCTCAAGCTCTTTA 90666
Qy 121 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 180
Db 90665 GGTTCGCAAAAGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 90606
Qy 181 TTCCGCTCGGATTCACGCGCTACAAAATCTATAAGCCCATCAACGATTTCAAACTT 240
Db 90605 TTCCGCTCGGATTCACGCGCTACAAAATCTATAAGCCCATCAACGATTTCAAACTT 90546
Qy 241 TACAGCATCGGCGCTCGCCATTTACGACTTCGACACCCCAATCGCCGTCACAAACCGTAT 300
Db 90545 TACAGCATCGGCGCTCGCCATTTACGACTTCGACACCCCAATCGCCGTCACAAACCGTAT 90486
Qy 301 CTCGGCGCGCTTGAGCTCAACCGGCTCCGTCGACTTGAGCGGCGAGCAGAGCTTC 360
Db 90485 CTCGGCGCGCTTGAGCTCAACCGGCTCCGTCGACTTGAGCGGCGAGCAGAGCTTC 90426
Qy 361 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 420
Db 90425 AGCCAAACCTCCATCGGCTCGGCGTATTGACGGGCGTAAAGCTATGCGGTTACCCCGAAT 90366
Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480
Db 90365 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 90306
Qy 481 GTCGCTTCGCGCAACTGTCCGTCGGGTCGGCGTCAAAATTCGA 525
Db 90305 GTCGCTTCGCGCAACTGTCCGCGGTCGGGTCGAAATTCGA 90261

RESULT 9
AAF21608/c
ID AAF21608 standard; DNA; 349980 BP.
```

XX AAF21608;  
 AC 13-MAR-2001 (first entry)  
 DT  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.  
 XX  
 KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;  
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;  
 KW ds.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 FN WO200066791-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005928.  
 XX  
 PR 30-APR-1999; 99US-0132068P.  
 PR 08-OCT-1999; 99WO-US023573.  
 PR 28-FEB-2000; 2000GB-00004695.  
 XX  
 XX (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;  
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
 PI Rappuoli R, Frazer CM, Grandi G;  
 XX  
 DR WPI; 2000-647603/62.  
 XX  
 XX Neisseria meningitidis B full length genome sequence and open reading  
 PT frames are used to detect, treat and prevent Neisserial infections.  
 XX  
 ES Claim 7; Appendix A; 692pp; English.  
 XX  
 CC The present invention describes the full length genome of Neisseria  
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613  
 CC represent fragments of the NMB genomic sequence, as the sequence was too  
 CC long to go in a record on its own it was split into 8 sequences which  
 CC overlap each other at the beginning and end of each sequence by 49980 bp  
 CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of  
 CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of  
 CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins  
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR  
 CC primers which are used in the exemplification of the present invention.  
 CC The NMB genome and fragments from it have antibacterial activity, and can  
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins  
 CC and/or antibodies which binds to the proteins can be used in compositions  
 CC for treating or preventing infection due to Neisserial bacteria or as a  
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or  
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,  
 CC computer storage medium or computer databases can be used in a search to  
 CC identify open reading frames (ORFs) or coding sequences within the NMB  
 CC genome. The DNA sequences provide further opportunities to find antigenic  
 CC or immunogenic proteins which are more effective in vaccines than the  
 CC outer membrane proteins currently used  
 XX  
 SQ Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;  
 Query Match 99.4%; Score 521.8; DB 3; Length 349980;  
 Best Local Similarity 99.6%; Pred. No. 1.6e-123;  
 Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ATGAAAAAGCACTTGCACACTGATGCTCTCCGCGCGCGCACTGCGGAA 60  
 DB 90786 ATGAAAAAGCACTTGCACACTGATGCTCTCCGCGCGCGCACTGCGGAA 90727  
 QY 61 GCGCGATCCGCTTTTACGTCCAGCCGATGCGCGCACACGCAAAAGCTCTCAAGCTCTTTA 120  
 DB 90726 GCGCGATCCGCTTTTACGTCCAGCCGATGCGCGCACACGCAAAAGCTCTCAAGCTCTTTA 90667

QY 121 GGTTCTGCCAAGGCTTCAGCCCG  
 DB 90666 GGTTCTGCCAAGGCTTCAGCCCG  
 QY 181 TTCCGCGTGCATTACAGCGCTACAAA  
 DB 90606 TTCCGCGTGCATTACAGCGCTACAAA  
 QY 241 TACAGCATCGCGCGTTCGCCATTACCG  
 DB 90546 TACAGCATCGCGCGTTCGCCATTACCG  
 QY 301 CTCCGCGCGCGCTTGAGCCTCAACCGCGCC  
 DB 90486 CTCCGCGCGCGCTTGAGCCTCAACCGCGCC  
 QY 361 AGCCAAACCTCCATCGCGCTCGGGGTATTGAC  
 DB 90426 AGCCAAACCTCCATCGCGCTCGGGGTATTGAC  
 QY 421 GTCGATTTGGATCGCGCTACCGCTACAACTPACI  
 DB 90366 GTCGATTTGGATCGCGCTACCGCTACAACTPACI  
 QY 481 GTCGCTTCGCGCGAAGCTGTCGCGCGTGCAGCTCAAAATCTGA 525  
 DB 90306 GTCGCTTCGCGCGAAGCTGTCGCGCGTGCAGCTCAAAATCTGA 90262  
 RESULT 10  
 AAT39041  
 ID AAT39041 standard; DNA; 850 BP.  
 AC AAT39041;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 22-DEC-1996 (first entry)  
 XX  
 DE Proteinase K resistant N. meningitidis 22 kD surface protein  
 KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae,  
 KW antibody; detection; probe; surface protein; ss.  
 XX  
 OS Neisseria meningitidis; strain Z4063.  
 XX  
 FH Key Location/Qualifiers  
 CDS 208..732  
 FT sig\_peptide /\*tag= a  
 FT 208..264 /\*tag= b  
 FT mat\_peptide 265..729 /\*tag= c  
 FT  
 XX WO9629412-A1.  
 FN  
 XX 26-SEP-1996.  
 PD  
 XX 15-MAR-1996; 96WO-CA000157.  
 XX  
 PR 17-MAR-1995; 95US-00406362.  
 PR 04-AUG-1995; 95US-0001983P.  
 XX  
 PA (IAPB-) IAP BIO VAC INC.  
 XX  
 PI Brodeur BR, Martin D, Hamel J, Rioux C;  
 XX  
 DR WPI; 1996-443187/44.  
 DR P-PSDB; AAW04893.  
 XX  
 PT Neisseria meningitidis antigen, highly conserved between different  
 PT strains - useful for prodn. of antibodies for immunisation against, or  
 PT diagnosis of, N. meningitidis infection.  
 XX

PS Claim 12; Fig 9; 117pp; English.

XX A proteinase K resistant surface protein has been isolated from 4 strains

CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,

CC antigenic fragments of antibodies can be used in a vaccine for the

CC prevention of infection by N. meningitidis or by N. gonorrhoeae in

CC humans. The antibodies may also be used diagnostically to detect N.

CC meningitidis infection. The antigen may also be used to detect antibodies

CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,

CC or their fragments, can be used as probes for the detection of pathogenic

CC Neisseria bacteria. (Updated on 16-Oct-2003 to standardise OS field)

XX

SQ Sequence 850 BP; 208 A; 273 C; 185 G; 184 T; 0 U; 0 Other;

Query Match 98.8%; Score 518.6; DB 2; Length 850;

Best Local Similarity 99.2%; Pred. No. 2.6e-123; Indels 0; Gaps 0;

Matches 521; Conservative 0; Mismatches 4;

Y 1 ATGAAAAAGCATTGGCCACACTGATTCGCTCTCCGCGCGCGCACTGGCGGAA 60

208 ATGAAAAAGCATTGGCCACACTGATTCGCTCTCCGCGCGCGCACTGGCGGAA 267

Y 61 GCGCATCCGGCTTTTACGTCGACGCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 120

268 GCGCATCCGGCTTTTACGTCGACGCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 327

Y 121 GGTCTCGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 180

328 GGTCTCGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 387

Y 181 TTGCGCGTCGATTACAGCGCTACAAAACTATTAAGCCCATCCACCGATTTCAAACTT 240

388 TTGCGCGTCGATTACAGCGCTACAAAACTATTAAGCCCATCCACCGATTTCAAACTT 447

Y 241 TACAGCATCGCGCGTCCGCAATTAGCATTCGACACCCCAATCCGCGTCAAAACCGTAT 300

448 TACAGCATCGCGCGTCCGCAATTAGCATTCGACACCCCAATCCGCGTCAAAACCGTAT 507

Y 301 CTGCGCGCGCTTGGAGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTC 360

508 CTGCGCGCGCTTGGAGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTC 567

Y 361 AGCCAAACCTCCACCGGCTCGGCTATTTGACGGGCGTAAAGCTATGCGGTTACCCGAA 420

568 AGCCAAACCTCCACCGGCTCGGCTATTTGACGGGCGTAAAGCTATGCGGTTACCCGAA 627

Y 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATTCGCAAAAGTCAACATGTCAAAAC 480

628 GTCGATTTGGATGCGGCTACCGCTACAACTACATTCGCAAAAGTCAACATGTCAAAAC 687

Y 481 GTCCGTTCCGCGAACTGTCCGTCGGGCTGCGCTCAAAATTTCTGA 525

688 GTCCGTTCCGCGAACTGTCCGTCGGGCTGCGCTCAAAATTTCTGA 732

RESULT 11

AB567381

ID AB567381 standard; DNA; 710 BP.

XX

AC AB567381;

XX

DT 29-NOV-2002 (first entry)

XX

DE Neisseria gonorrhoeae outer membrane gene #1.

XX

KW Gram-negative bacterial bleb; PorB; outer membrane protein;

KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;

KW protective antigen; antibacterial; vaccine; gene; ds.

XX

OS Neisseria gonorrhoeae.

XX

FN W0200262380-A2

XX

PD 15-AUG-2002.

XX

PP 08-FEB-2002; 2002WO-EP001356.

XX

PR 08-FEB-2001; 2001GB-00003169.

XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX

PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;

XX

XX WPI; 2002-657510/70.

DR P-PSDB; ABG91063.

XX

PT Novel gram-negative bacterial bleb presenting on its surface PorB outer

PT membrane protein from Chlamydia trachomatis or protective antigen from

PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.

XX

PS Disclosure; Page 54; 75pp; English.

XX

CC The present invention relates to a new gram-negative bacterial bleb

CC presenting on its surface the PorB outer membrane protein from Chlamydia

CC trachomatis, or a protective antigen from C. pneumoniae. The invention is

CC useful for preventing C. trachomatis or C. pneumoniae infection in a

CC host. The present nucleic acid sequence represents a Neisseria

CC gonorrhoeae gene as described in the invention

XX

SQ Sequence 710 BP; 171 A; 228 C; 160 G; 151 T; 0 U; 0 Other;

Query Match 95.7%; Score 502.6; DB 6; Length 710;

Best Local Similarity 97.3%; Pred. No. 3.2e-119;

Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Y 1 ATGAAAAAGCATTGGCCACACTGATTCGCTCTCCGCGCGCGCACTGGCGGAA 60

141 ATGAAAAAGCATTGGCCACACTGATTCGCTCTCCGCGCGCGCACTGGCGGAA 200

Y 61 GCGCATCCGGCTTTTACGTCGACGCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 120

201 GCGCATCCGGCTTTTACGTCGACGCGATGCCGACACGCAAAAGCTCAAGCTCTTTA 260

Y 121 GGTCTCGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 180

261 GGTCTCGCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 320

Y 181 TTGCGCGTCGATTACAGCGCTACAAAACTATTAAGCCCATCCACCGATTTCAAACTT 240

321 TTGCGCGTCGATTACAGCGCTACAAAACTATTAAGCCCATCCACCGATTTCAAACTT 380

Y 241 TACAGCATCGCGCGTCCGCAATTACGATTCGACACCCCAATCCGCGTCAAAACCGTAT 300

381 TACAGCATCGCGCGTCCGCAATTACGATTCGACACCCCAATCCGCGTCAAAACCGTAT 440

Y 301 CTGCGCGCGCTTGGAGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTC 360

441 CTGCGCGCGCTTGGAGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTC 500

Y 361 AGCCAAACCTCCACCGGCTCGGCTATTTGACGGGCGTAAAGCTATGCGGTTACCCGAA 420

501 AGCCAAACCTCCACCGGCTCGGCTATTTGACGGGCGTAAAGCTATGCGGTTACCCGAA 567

Y 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATTCGCAAAAGTCAACATGTCAAAAC 525

561 GTCGATTTGGATGCGGCTACCGCTACAACTACATTCGCAAAAGTCAACATGTCAAAAC 621

621 GTCGATTTGGATGCGGCTACCGCTACAACTACATTCGCAAAAGTCAACATGTCAAAAC 687

RESULT 12

AAT39042

ID AAT39042 standard; DNA; 810 BP

XX

AC AAT39042;  
 XX 16-OCT-2003 (revised)  
 DT 22-DEC-1996 (first entry)  
 XX  
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.  
 XX  
 XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
 KW antibody; detection; probe; surface protein; ss.  
 XX  
 OS Neisseria meningitidis; strain b2.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 241..765  
 FT /\*tag= a  
 FT sig\_peptide 241..297  
 FT /\*tag= b  
 FT sig\_peptide 298..762  
 FT /\*tag= c  
 XX  
 PN WO9629412-A1.  
 XX  
 XX 26-SEP-1996.  
 XX  
 PF 15-MAR-1996; 96WO-CA000157.  
 XX  
 PR 17-MAR-1995; 95US-00406362.  
 PR 04-AUG-1995; 95US-0001983P.  
 XX  
 PA (IAFB-) IAF BIO VAC INC.  
 XX  
 PI Brodeur BR, Martin D, Hamel J, Rioux C;  
 XX  
 XX WPI; 1996-443187/44.  
 DR P-PSDB; AAW04894.  
 DR  
 XX Neisseria meningitidis antigen, highly conserved between different  
 PT strains - useful for prodn. of antibodies for immunisation against, or  
 PT diagnosis of, N. meningitidis infection.  
 XX  
 PS Claim 12; Fig 10; 117pp; English.  
 XX  
 XX A proteinase K resistant surface protein has been isolated from 4 strains  
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,  
 CC antigenic fragments of antibodies can be used in a vaccine for the  
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in  
 CC humans. The antibodies may also be used diagnostically to detect N.  
 CC meningitidis infection. The antigen may also be used to detect antibodies  
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,  
 CC or their fragments, can be used as probes for the detection of pathogenic  
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 810 BP; 186 A; 260 C; 186 G; 178 T; 0 U; 0 Other;  
 Query Match 95.7%; Score 502.6; DB 2; Length 810;  
 Best Local Similarity 97.3%; Pred. No. 3.3e-119;  
 Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 ATGAAAAAGCACTTGGCCACACTGATGCTCTCCGCTCTCCGCGCGCGCACTGGCGGAA 60  
 DB 241 ATGAAAAAGCACTTGGCCACACTGATGCTCTCCGCTCTCCGCGCGCGCACTGGCGGAA 300  
 QY 61 GCGCATCCGGCTTTTACGTCCAAAGCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 DB 301 GCGCATCCGGCTTTTACGTCCAAAGCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 QY 121 GGTCTGCAAGGCTTTCAGCGCGCGGCGATCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 DB 361 GGTCTGCAAGGCTTTCAGCGCGCGGCGATCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 QY 181 TTGCGCGGTGATATACCGCGGTACAAAACATATAAAGCCCGGCGGCGGCGGCGGCGGCGGCGG 240  
 DB 421 TTGCGCGGTGATATACCGCGGTACAAAACATATAAAGCCCGGCGGCGGCGGCGGCGGCGGCGG 480

QY 241 TACAGCATCGGCGGTCCGCCATTTACGACTTTCGACACCCCAATCCCGTCAAAACCGTAT 300  
 DB 481 TACAGCATCGGCGGTCCGCCATTTACGACTTTCGACACCCCAATCCCGTCAAAACCGTAT 540  
 QY 301 CTCGGCGCGCGCTTGAGCCTCAACCGCGCTCCGCTCGACTTGGCGGCGGCGGCGGCGGCTTC 360  
 DB 541 TTCCGCGCGCGCTTGAGCCTCAACCGCGCTTCCGCCCACTTGGCGGCGGCGGCGGCGGCGGCTTC 600  
 QY 361 AGCCAAACCTCCATCGGCGCTCGGCTATTGACGGCGGTAAGCTATGCGGTTACCCCGAAT 420  
 DB 601 AGCAAAACCTCCGCGCGCTCGGCTATTGCGGCGGCTAGCTATGCGGTTACCCCGAAT 560  
 QY 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGCAAAAGTCAACACTGTCTCAAAAAC 480  
 DB 661 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGCGGCAAAAGTCAACACTGTCTCAAAAAC 720  
 QY 481 GTCGCTTCCGCGCAACTGCTCGGCGGCTCGGCTCAAAATTCGA 525  
 DB 721 GTCGCTTCCGCGCAACTGCTCGGCGGCTCGGCTCAAAATTCGA 765  
 RESULT 13  
 AAT39040  
 ID AAT39040 standard; DNA; 710 BP.  
 AC AAT39040;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 22-DEC-1996 (first entry)  
 XX  
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.  
 XX  
 KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
 KW antibody; detection; probe; surface protein; ss.  
 XX  
 OS Neisseria meningitidis; strain MCH88.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 116..643  
 FT /\*tag= a  
 FT sig\_peptide 116..172  
 FT /\*tag= b  
 FT mat\_peptide 173..640  
 FT /\*tag= c  
 XX  
 PN WO9629412-A1.  
 XX  
 PD 26-SEP-1996.  
 XX  
 PF 15-MAR-1996; 96WO-CA000157.  
 XX  
 PR 17-MAR-1995; 95US-00406362.  
 PR 04-AUG-1995; 95US-0001983P.  
 XX  
 PA (IAFB-) IAF BIO VAC INC.  
 XX  
 PI Brodeur BR, Martin D, Hamel J, Rioux C;  
 XX  
 XX WPI; 1996-443187/44.  
 DR P-PSDB; AAW04892.  
 DR  
 XX Neisseria meningitidis antigen, highly conserved between different  
 PT strains - useful for prodn. of antibodies for immunisation against, or  
 PT diagnosis of, N. meningitidis infection.  
 XX  
 PS Claim 12; Fig 8; 117pp; English.  
 XX  
 XX A proteinase K resistant surface protein has been isolated from 4 strains  
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,  
 CC antigenic fragments of antibodies can be used in a vaccine for the  
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in  
 CC humans. The antibodies may also be used diagnostically to detect N.



CC meningitis infection. The antigen may also be used to detect antibodies  
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,  
 CC or their fragments, can be used as probes for the detection of pathogenic  
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 710 BP; 174 A; 232 C; 148 G; 156 T; 0 U; 0 Other;  
 Query Match 93.6%; Score 491.2; DB 2; Length 710;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-116;  
 Matches 512; Conservative 0; Mismatches 13; Indels 3; Gaps 1;  
 Qy 1 ATGAAAAGACCTTGCCACACTGATGCTCCCTCTCTCCGCGCGGCACTGGCGAA 60  
 Db 116 ATGAAAAGACCTTGCCACACTGATGCTCCCTCTCCGCGCGGCACTGGCGAA 175  
 Qy 61 GGCGCATCCGCTTTAGTCCAGCCGATGCGCACAGCAAGCAAGCTCAAGCTCTTTA 120  
 Db 176 GGCGCATCCGCTTTAGTCCAGCCGATGCGCACAGCAAGCTCAAGCTCTTTA 235  
 Qy 121 GGTTCGCAAGCTTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCTCCGC 180  
 Db 236 GGTTCGCAAGCTTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCTCCGC 295  
 Qy 181 TTCGCGTCTGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACGATTTCAA 237  
 Db 296 TTCGCGTCTGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACGATTTCAA 355  
 Qy 238 CTTTACAGCATCGGCGTCCGCACTTACGACTTCGACCCCAATCCCGTCAACCG 297  
 Db 356 CTTTACAGCATCGGCGTCCGCACTTACGACTTCGACCCCAATCCCGTCAACCG 415  
 Qy 298 TATCTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGAGCAGC 357  
 Db 416 TATCTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGAGCAGC 475  
 Qy 358 TTCAGCAAACTCCATCGGCTCGGCGTATTGACGGCGTAAAGCTATGCCGTTACCCG 417  
 Db 476 TTCAGCAAACTCCATCGGCTCGGCGTATTGACGGCGTAAAGCTATGCCGTTACCCG 535  
 Qy 418 AATGTCGATTTGGATGCGGCTACGCTACAACTACATCGGCAAGTCAACACTGTCAA 477  
 Db 536 AATGTCGATTTGGATGCGGCTACGCTACAACTACATCGGCAAGTCAACACTGTCAA 595  
 Qy 478 AAGTCCGTTCCGCGAACTGTCCGTCGGCGTGGCGTCAAAATTCGA 525  
 Db 596 AATGTCGTTCCGCGAACTGTCCGTCGGCGTGGCGTCAAAATTCGA 643

RESULT 14  
 ABZ38961  
 ID ABZ38961 standard; DNA; 525 BP.

XX AC ABZ38961;

XX DT 07-MAR-2003 (first entry)

XX DE N. gonorrhoeae nucleotide sequence SEQ ID 2511.

XX KW Antibacterial; infection; vaccine; gene therapy; gene; ds.

XX OS Neisseria gonorrhoeae.

XX PN W0200279243-A2.

XX FD 10-OCT-2002.

XX PF 12-FEB-2002; 2002WO-IB002069.

XX PR 12-FEB-2001; 2001GB-00003424.

XX PA (CHIR-) CHIRON SPA.

XX PI Fontana MR, Pizza M, Masignani V, Monaci E;

XX DR

WPI; 2003-058415/05.

DR P-PSDB; ABP77991.

XX PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
 PT medicament for treating or preventing N. gonorrhoeae infection.

XX PS Disclosure; Page 371; 815pp; English.

XX CC The present invention relates to proteins from Neisseria gonorrhoeae.  
 CC Also disclosed are the nucleic acid molecules encoding the proteins and  
 CC antibodies that specifically bind to the proteins. The composition  
 CC comprising the protein, nucleic acid or antibody is useful for the  
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
 CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid  
 CC molecules of the invention

XX SQ Sequence 525 BP; 117 A; 188 C; 120 G; 100 T; 0 U; 0 Other;

Query Match 91.5%; Score 480.2; DB 10; Length 525;

Best Local Similarity 96.0%; Pred. No. 1.7e-113;

Matches 504; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Qy 1 ATGAAAAGACCTTGCCACACTGATGCTCCCTCTCCGCGCGGCACTGGCGAA 60

Db 1 ATGAAAAGACCTTGCCACACTGATGCTCCCTCTCCGCGCGGCACTGGCGAA 60

Qy 61 GGCGCATCCGCTTTAGTCCAGCCGATGCGCACAGCAAGCAAGCTCAAGCTCTTTA 120

Db 61 GGCGCATCCGCTTTAGTCCAGCCGATGCGCACAGCAAGCTCAAGCTCTTTA 120

Qy 121 GGTTCGCAAGCTTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCTCCGC 180

Db 121 GGTTCGCAAGCTTTCAGCCCGCATCTCCGAGGCTACCGCATCAAGCTCCGC 180

Qy 181 TTCGCGTCTGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACGATTTCAA 237

Db 181 TTCGCGTCTGATTACAGCGCTACAAAAAATATA---AAGCCCATCCACGATTTCAA 240

Qy 238 CTTTACAGCATCGGCGTCCGCACTTACGACTTCGACCCCAATCCCGTCAACCG 297

Db 241 CTTTACAGCATCGGCGTCCGCACTTACGACTTCGACCCCAATCCCGTCAACCG 300

Qy 298 TATCTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGAGCAGC 357

Db 301 TATCTCGGCGCGCTTGAGCTCAACCGCGCTCCGTCGACTTTGGGCGGAGCAGC 360

Qy 358 TTCAGCAAACTCCATCGGCTCGGCGTATTGACGGCGTAAAGCTATGCCGTTACCCG 417

Db 361 TTCAGCAAACTCCATCGGCTCGGCGTATTGACGGCGTAAAGCTATGCCGTTACCCG 420

Qy 418 AATGTCGATTTGGATGCGGCTACGCTACAACTACATCGGCAAGTCAACACTGTCAA 477

Db 421 AATGTCGATTTGGATGCGGCTACGCTACAACTACATCGGCAAGTCAACACTGTCAA 480

Qy 478 AAGTCCGTTCCGCGAACTGTCCGTCGGCGTGGCGTCAAAATTC 522

Db 481 AAGTCCGTTCCGCGAACTGTCCGTCGGCGTGGCGTCAAAATTC 525

RESULT 15

ADL13425

ID ADL13425 standard; DNA; 468 BP.

XX AC ADL13425;

XX DT 03-JUN-2004 (first entry)

XX DE Neisseria meningitidis H44/76 mature NapA-encoding DNA.

XX KW Neisseria surface protein A; NapA; refolding; recombinant production;  
 KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;

KW invasive bacterial disease; bacteraemia; meningitis;  
 KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;  
 KW antibacterial; gene therapy; gene; ds.  
 XX Neisseria meningitidis; H44/76.

OS  
 FH Key Location/Qualifiers  
 FT CDS 1..468  
 FT /tag= b  
 FT /partial  
 FT /product= "Mature NspA"  
 FT /note= "No start codon given"  
 FT mat\_peptide 1..465  
 FT /tag= a  
 FT /product= "Mature NspA"

XX WO2004020452-A2.

PD 11-MAR-2004.

XX 28-AUG-2003; 2003WO-EP010085.

XX 30-AUG-2002; 2002GB-00020197.

XX (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA.  
 XX (UYUT-) RIJKSUNIV UTRECHT.

XX Biemans R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;  
 XX Tommassen J, Weynants V;

XX WPI; 2004-239150/22.

DR P-ESDB; ADL13426.

XX New refolded NspA protein, useful for preparing a composition for  
 PT diagnosing, treating or preventing infection caused by Neisseria  
 PT meningitidis or Neisseria gonorrhoeae.

XX Example 1; Fig 2; 62pp; English.

XX The invention relates to an isolated refolded Neisserial surface protein  
 CC A (NspA) from Neisseria meningitidis or Neisseria gonorrhoeae. The  
 CC invention also relates to the method of refolding an NspA protein; an  
 CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-  
 CC dimethyldecylammonioethanesulphonate) for refolding an NspA protein; a  
 CC pharmaceutical composition comprising the refolded NspA protein, a  
 CC carrier and optionally one or more other Neisserial antigens; a method of  
 CC preventing or treating a Neisserial infection; an antibody immunospecific  
 CC for the NspA protein; and diagnosing a Neisserial infection. NspA has  
 CC characteristics which indicate that it is a potential vaccine candidate  
 CC for the development of subunit vaccines for the treatment of infections  
 CC caused by Neisseria meningitidis (meningococcus), which causes invasive  
 CC bacterial diseases such as bacteraemia and meningitis, or Neisseria  
 CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced  
 CC NspA could therefore be used to produce vaccine compositions and it could  
 CC also be used in the development of new antimicrobial agents, diagnostic  
 CC tests and in drug screening. However, recombinantly produced proteins are  
 CC frequently unable to adopt their biologically active conformations, and  
 CC yields may be very low due to mis-folding and aggregation of the protein.  
 CC The method of the invention provides an improved method for refolding the  
 CC NspA protein, and it is possible to increase the recovery of active  
 CC protein form partly purified inclusion bodies in amounts up to 100%  
 CC without the need for further purification. The refolded NspA protein is  
 CC useful for preparing a composition for diagnosing, treating or preventing  
 CC infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The  
 CC present sequence represents DNA encoding the mature NspA protein from  
 CC Neisseria meningitidis H44/76 which was amplified and cloned in an  
 CC example of the invention.

SQ Sequence 468 BP; 105 A; 164 C; 106 G; 93 T; 0 U; 0 Other;

Query Match 88.5%; Score 464.8; DB 12; Length 468;  
 Best Local Similarity 99.6%; Pred. NO. 1.5e-109;  
 Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCGCATCCGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCCTCAAGCTCT 117  
 DB 1 GAAGCGCATCCGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCCTCAAGCTCT 60  
 QY 118 TTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTC 177  
 DB 61 TTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTC 120  
 QY 178 CGCTTCGCGCTCGATTACACGCGCTACAAAACCTATAAAGCCCCCATCCACCGATTTCAAA 237  
 DB 121 CGCTTCGCGCTCGATTACACGCGCTACAAAACCTATAAAGCCCCCATCCACCGATTTCAAA 180  
 QY 238 CTTTACAGCATCGCGCGCTCCGCCATTTCACGCTTCGACACCCCAATCGCCGTCAAAACCG 297  
 DB 181 CTTTACAGCATCGCGCGCTCCGCCATTTCACGCTTCGACACCCCAATCGCCGTCAAAACCG 240  
 QY 298 TATCTCGCGCGCGCTTGAGGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGC 357  
 DB 241 TATCTCGCGCGCGCTTGAGGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGC 300  
 QY 358 TTACGCCAAACCTCCATCGGCTCGGCGTATTGACGGCGCTAAGCTATGCGGTACCCCG 417  
 DB 301 TTACGCCAAACCTCCATCGGCTCGGCGTATTGACGGCGCTAAGCTATGCGGTACCCCG 360  
 QY 418 AATGTGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCTCAA 477  
 DB 361 AATGTGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCTCAA 420  
 QY 478 AACGTTCGTTCCGGGGAACCTGTCGTCGGCGTGGCGTCAAAATTTCTGA 525  
 DB 421 AACGTTCGTTCCGGGGAACCTGTCGTCGGCGTGGCGTCAAAATTTCTGA 468

Search completed: January 12, 2006, 20:20:03  
 Job time : 494 secs



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 20:10:48 ; Search time 161 Seconds  
(without alignments)  
5796.397 Million cell updates/sec

Title: US-10-650-123-1  
Perfect score: 525  
Sequence: 1 atgaaaaagcactgtccac.....gcgtgcgcgtcaaatctga 525

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgm2\_6/ptodata/1/ina/1\_COMB.seq.\*
- 2: /cgm2\_6/ptodata/1/ina/5\_COMB.seq.\*
- 3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgm2\_6/ptodata/1/ina/H\_COMB.seq.\*
- 6: /cgm2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 7: /cgm2\_6/ptodata/1/ina/PP\_COMB.seq.\*
- 8: /cgm2\_6/ptodata/1/ina/RE\_COMB.seq.\*
- 9: /cgm2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	518.6	98.8	850	3	US-08-913-362-5
3	502.6	95.7	810	3	US-08-913-362-7
4	501.2	95.5	528	3	US-08-913-362-29
5	491.2	93.6	710	3	US-08-913-362-3
6	49.8	9.5	1919	3	US-09-614-912-175
7	45.6	8.7	4403765	3	US-09-103-840A-2
8	45.6	8.7	4411529	3	US-09-103-840A-1
9	45	8.6	4403765	3	US-09-103-840A-2
10	45	8.6	4411529	3	US-09-103-840A-1
11	44	8.4	1082	3	US-09-881-165-4
12	44	8.4	4483	3	US-08-961-527-363
13	44	8.4	32768	3	US-08-961-527-71
14	43.6	8.3	390	3	US-09-197-649-7
15	43	8.2	925	3	US-08-858-003-1
16	43	8.2	925	3	US-09-078-166-1
17	43	8.2	925	3	US-08-997-467-1
18	42.8	8.2	2434	3	US-09-902-540-3527
19	42.8	8.2	18538	3	US-09-902-540-1169
20	42.4	8.1	36519	3	US-08-923-137-2
21	42	8.0	620	3	US-08-961-527-374
22	42	8.0	1859	3	US-08-894-818B-15
23	42	8.0	1859	3	US-08-841-553-15
24	42	8.0	1977	3	US-08-894-818B-2

25	42	8.0	1977	3	US-08-894-818B-6	Sequence 6, Appli
26	42	8.0	1977	3	US-09-445-472-11	Sequence 11, Appli
27	42	8.0	1977	3	US-10-090-624-11	Sequence 11, Appli
28	42	8.0	1977	3	US-09-841-553-2	Sequence 2, Appli
29	42	8.0	1977	3	US-09-841-553-6	Sequence 6, Appli
30	41.6	7.9	867	3	US-09-216-333B-340	Sequence 340, App
31	41.6	7.9	867	3	US-09-216-333B-342	Sequence 342, App
32	41.6	7.9	1397	3	US-09-216-333B-343	Sequence 343, App
33	41.6	7.9	1397	3	US-09-216-333B-345	Sequence 345, App
34	41.4	7.9	1614	3	US-09-489-039A-3484	Sequence 3484, Ap
35	41.4	7.9	1698	3	US-09-489-039A-3505	Sequence 3505, Ap
36	41.4	7.9	1706	3	US-10-033-109-3	Sequence 3, Appli
37	41.4	7.9	3486	3	US-09-614-221A-292	Sequence 292, App
38	41.4	7.9	25254	3	US-09-902-540-1233	Sequence 1233, Ap
39	41.4	7.9	58857	3	US-09-477-962-1	Sequence 1, Appli
40	41.2	7.8	1781	3	US-09-675-018B-7	Sequence 7, Appli
41	41.2	7.8	1781	3	US-10-428-041-7	Sequence 7, Appli
42	41.2	7.8	1889	3	US-09-675-018B-9	Sequence 9, Appli
43	41.2	7.8	1889	3	US-10-428-041-9	Sequence 9, Appli
44	41	7.8	1439	3	US-09-056-556-167	Sequence 167, App
45	41	7.8	1439	3	US-09-072-596-162	Sequence 162, App

## ALIGNMENTS

RESULT 1  
US-08-913-362-1  
; Sequence 1, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josée  
; APPLICANT: Rioux, Clément  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913.362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406.362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001.983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 830 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 143..667
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 143..199
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 200..667
US-08-913-362-1

Query Match 100.0%; Score 525; DB 3; Length 830;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAGACATGCGCACACTGATGCGCTCGCTCTCCGGCGCGCGCACTGGCGGAA 60
Db 143 ATGAAAAGACATGCGCACACTGATGCGCTCTCCGGCGCGCGCACTGGCGGAA 202

Qy 61 GCGCATCCGGCTTTTACGTCCAGCCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 120
Db 203 GCGCATCCGGCTTTTACGTCCAGCCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 262

Qy 121 GTTCTGCAAGGGTTGAGCGCGGATCTCCGAGGCTACCGGATCAAGACTTCGCG 180
Db 263 GTTCTGCAAGGGTTGAGCGCGGATCTCCGAGGCTACCGGATCAAGACTTCGCG 322

Qy 181 TTCGGCTCGATTACACGGCTACAAAACTATAAAGCCCATCCACCGATTTCAAACTT 240
Db 323 TTCGGCTCGATTACACGGCTACAAAACTATAAAGCCCATCCACCGATTTCAAACTT 382

Qy 241 TACAGCATCGCGCTCGCGCATTTACGACTTCGACACCAATCGCCCGTCAAAACCGTAT 300
Db 383 TACAGCATCGCGCTCGCGCATTTACGACTTCGACACCAATCGCCCGTCAAAACCGTAT 442

Qy 301 CTGGCGCGCGCTGAGCTCAACCGCGCTCGCTCGCTGAGCTTTGGGCGGAGGACAGTTTC 360
Db 443 CTGGCGCGCGCTGAGCTCAACCGCGCTCGCTCGCTGAGCTTTGGGCGGAGGACAGTTTC 502

Qy 361 AGCCAAACCTCATCGGCTCGGCTATTGAGGGCGTAAGCTATGCCGTTACCCCGAAT 420
Db 503 AGCCAAACCTCATCGGCTCGGCTATTGAGGGCGTAAGCTATGCCGTTACCCCGAAT 562

Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 480
Db 563 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 622

Qy 481 GTCGCTTCGGCGCAACTGCTCGCTGGCGTGGCGGTCGAAATTCGA 525
Db 623 GTCGCTTCGGCGCAACTGCTCGCTGGCGTGGCGGTCGAAATTCGA 667

RESULT 2
US-08-913-362-5
; Sequence 5, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
```

```
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/POCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: Z4063
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 208..732
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 208..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..732
US-08-913-362-5
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Query Match 98.8%; Score 518.6; DB 3; Length 850;
Best Local Similarity 99.2%; Pred. No. 6.8e-130;
Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAAAAGACATGCGCACACTGATGCGCTCTCCGGCGCGCGCACTGGCGGAA 60
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Qy 61 GCGCATCCGGCTTTTACGTCCAGCCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 120
Db 268 GCGCATCCGGCTTTTACGTCCAGCCGATGCGCACACGCAAAAGCCTCAAGCTCTTTA 327

Qy 121 GGTTCGCAAGGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGCG 180
Db 328 GGTTCGCAAGGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTTCGCG 387

Qy 181 TTCGGCTCGATTACACGGCTACAAAATATATAAGCCCATCCACCGATTTCAAACTT 240
Db 388 TTCGGCTCGATTACACGGCTACAAAATATATAAGCCCATCCACCGATTTCAAACTT 447

Qy 241 TACAGCATCGGCGGTCCGCCATTTACGACTTCGACACCCCAATCGCCGTCAAACCGTAT 300
Db 448 TACAGCATCGGCGGTCCGCCATTTACGACTTCGACACCCCAATCGCCGTCAAACCGTAT 507
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QY 301 CTCGGCGCGCTTGAAGCTCAACCGCGCTCCGTGACTTGGGCGGCGAGCGACAGCTTC 360  
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QY 481 GTCGTTCCGGCGAAGTGTCCGCGGTGGCGGTCAAAATTCGA 525  
Db 688 GTCGTTCCGGCGAAGTGTCCGCGGTGGCGGTCAAAATTCGA 732

RESULT 3

US-08-913-362-7  
; Sequence 7, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 13-NOV-1997  
; APPLICATION NUMBER: US/08/913.362  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406.362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001.983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 810 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Neisseria gonorrhoeae  
; STRAIN: b2  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 241..765

; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 241..297  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 298..765  
US-08-913-362-7  
Query Match 95.7%; Score 502.6; DB 3; Length 810;  
Best Local Similarity 97.3%; Pred. No. 1.3e-125;  
Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 ATGAAAAAGACATTGCCACATGATTGCCCTCTCCGCGCGCGCGACTGCGGAA 60  
Db 241 ATGAAAAAGACATTGCCGCACTGATTGCCCTCCGCACTCCGCGCGCGCACTGGCGGAA 300  
QY 61 GGCGCATCCGGCTTTTACGTCAAAGCGATGCCGACACGCAAGAAAGCTCAAGCTCTTTA 120  
Db 301 GGCGCATCCGGCTTTTACGTCAAAGCGATGCCGACACGCAAGAAAGCTCAAGCTCTTTA 360  
QY 121 GGTTCGCAAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180  
Db 361 GGTTCGCAAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 420  
QY 181 TTGCGCGTCGATTACACGCGCTACAAAACCTATAAAGCGCCATCCACCGATTCAACTT 240  
Db 421 TTGCGCGTCGATTACACGCGCTACAAAACCTATAAAGCGCCATCCACCGATTCAACTT 480  
QY 241 TACAGCATCGCGCGTCCGCCATTACGACTTCGACACCCCAATCCCGTCAAAACCGTAT 300  
Db 481 TACAGCATCGCGCGTCCGCCATTACGACTTCGACACCCCAATCCCGTCAAAACCGTAT 540  
QY 301 CTGCGCGCGCTTTGAGCTTCAACCGCGCTCCGTCGATCTTGGCGGCGAGCGACAGCTTC 360  
Db 541 TTGCGCGCGCTTTGAGCTTCAACCGCGCTCCGTCGATCTTGGCGGCGAGCGACAGCTTC 600  
QY 361 AGCAAACTCCATCGCGCTCGGCGTATTGAGCGGCGTAAAGCTATGCCGTTACCCCGAAT 420  
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QY 421 GTCGATTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 480  
Db 661 GTCGATTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAAC 720  
QY 481 GTCGTTCCGGCGAAGTGTCCGCGGTGGCGGTCAAAATTCGA 525  
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RESULT 4

US-08-913-362-29  
; Sequence 29, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 528 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "consensus"
US-08-913-362-29

Query Match 95.5%; Score 501.2; DB 3; Length 528;
Best Local Similarity 95.1%; Pred. No. 2.8e-125;
Matches 502; Conservative 22; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAAAAAGACATTGCCACACTGATTCGCCCTCGCTCTCCGGCGCGCGCACTGGCGGAA 60
DB 1 ATGAAAAAGACATTGCCACACTGATTCGCCCTCGCTCTCCGGCGCGCGCACTGGCGGAA 60
QY 61 GGGCGATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
DB 61 GGGCGATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA 120
QY 121 GGTTCGCAAGGCTTCAGCCCGGCTATCCGAGGCTACCGCATCAAGCACTCCGC 180
DB 121 GGTTCGCAAGGCTTCAGCCCGGCTATCCGAGGCTACCGCATCAAGCACTCCGC 180
QY 181 TTCGCGTCGATTACACGCGCTACAAAATATATA---AAGCCCATCCACCGATTTCAAA 237
DB 181 TTCGCGTCGATTACACGCGCTACAAAATATATAAAGGCTCCATCCACCGATTTCAAA 240
QY 238 CTTTACAGCATCGGCGCTCCGCCATTTCAGCTTCGACACCAATCGCCGTCAAACCG 297
DB 241 CTTTACAGCATCGGCGCTCCGCYCATTTACGACTTCGACACCAATCGCCGTCAAACCG 300
QY 298 TATTCGCGCGCTTGAGCTCAACCGCGCTCCGCTCGACTTGGCGGCGAGCAGC 357
DB 301 TATTCGCGCGCTTGAGCTCAACCGCGCTCCGCTCGACTTGGCGGCGAGCAGC 360
QY 358 TTACGCAAACTCCATCGGCTCGGCTATTCGAGCGGCTAAGCTATGCGGTTACCCCG 417
DB 361 TTACGCAAACTCCRYCGGCTCGGCTATTCGAGCGGCTAAGCTATGCGGTTACCCCG 420
QY 418 AATGTCGATTTGGATTCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAA 477
DB 421 AATGTCGATTTGGATTCGCGCTACCGCTACAACTACATTCGCAAGTCAACACTGTCAA 480
QY 478 AACGTCGCTTCGCGCACTCTCGCTCGGCTGCGGCTCAAAATCTGA 525
DB 481 AAYGTCGCTTCGCGCACTCTCGCTCGGCTGCGGCTCAAAATCTGA 528

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RESULT 5  
 US-08-913-362-3  
 ; Sequence 3, Application US/08913362  
 ; Patent No. 6287574  
 ; GENERAL INFORMATION:

```

; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: MCH88
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116..643
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 116..172
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 173..643
; US-08-913-362-3

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Query Match 93.6%; Score 491.2; DB 3; Length 710;  
 Best Local Similarity 97.0%; Pred. No. 1.5e-122;  
 Matches 512; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

QY	1	ATGAAAAAGACATTGCCACACTGATTCGCCCTCGCTCTCCGGCGCGCGCACTGGCGGAA	60
DB	116	ATGAAAAAGACATTGCCACACTGATTCGCCCTCGCTCTCCGGCGCGCGCACTGGCGGAA	175
QY	61	GGCGCATCCGGCTTTTACGTCCAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA	120
DB	176	GGCGCATCCGGCTTTTACGTCCAGCCGATGCGGCACACGCAAAAGCTCAAGCTCTTTA	235
QY	121	GGTTCTGCAAGGCTTCAGCCCGGCTATCCGAGGCTACCGCATCAAGCACTCCGC	180

Db 236 GGTTCGCCAAGGCTTCAGCCGCGCATCTCGAGGCTACCGCATCAAGCACTCCGC 295  
QY 181 TTGCGCGTCGATTAACGCGCTACAAAACCTATA---AAGCCCATCCACCGATTCAAA 237  
Db 296 TTGCGCGTCGATTAACGCGCTACAAAACCTATAAAAGTCCCATCCACCGATTCAAA 355  
QY 238 CTTTACAGCATCGGCGCTCGCCCATTTAGCACTTCGACACCAATCGCCGCTCAACCG 297  
Db 356 CTTTACAGCATCGGCGCTCGCCCATTTTACGATTCGACACCAATCCCGCTCAACCG 415  
QY 298 TATCTCGGCGCGCTTTAGCCTCAACCGCGCTCGTGCAGCTTGGGCGGCGAGACGC 357  
Db 416 TATCTCGGCGCGCTTTAGCCTCAACCGCGCTCGTGCAGCTTTTAAACGCGAGACGC 475  
QY 358 TTACGCAAACTCCATCGGCTCGCGCTATTGAAGCGGCTAAGCTATCGGTTACCCCG 417  
Db 476 TTACGCAAACTCCACCGCGCTCGCGCTATTGGGCGGCTAAGCTATCGGTTACCCCG 535  
QY 418 ATGTGCGATTTGATCGCGCTACCGCTCAACTACATCGGCAAGTCAAGCTGTCAAA 477  
Db 536 ATGTGCGATTTGATCGCGCTACCGCTCAACTACATCGGCAAGTCAAGCTGTCAAA 595  
QY 478 AAGTCCGCTTCGCGGCACTGTCCGTCGCGCTCGCGTCAAAATTTCTGA 525  
Db 596 AATGTCCTTCGCGGCACTGTCCGCGCGCTACCGCTCAAAATTTCTGA 643

RESULT 6

US-09-614-912-175  
; Sequence 175, Application US/09614912  
; Patent No. 6677502  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Orozco, Buddy  
; APPLICANT: Miao, Gou-Hau  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Lee, Jian Ming  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Wang, Zude  
; APPLICANT: Calmi, Perry G  
; APPLICANT: Anderson, Shawn  
; TITLE OF INVENTION: Plant Metabolism Genes  
; FILE REFERENCE: B1378 US NA  
; CURRENT APPLICATION NUMBER: US/09/614,912  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: 60/143,401  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/143,412  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/146,650  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 60/170,906  
; PRIOR FILING DATE: 1999-12-15  
; PRIOR APPLICATION NUMBER: 60/172,959  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/172,946  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 175  
; LENGTH: 1919  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-09-614-912-175

Query Match 9.5%; Score 49.8; DB 3; Length 1919;  
Best Local Similarity 49.8%; Pred. No. 0.001;  
Matches 126; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 125 CTGCCAAGGCTTCAGCGCGCGCATCTCGCGAGGCTACCGCATCAAGCACTCCGCTTGG 184  
Db 396 CCGCCTACCGCGCTTCCTCACCATCGGCGAGCCCACTGGAGCAGCAACGCTCTACTCGC 455

RESULT 7

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 8.7%; Score 45.6; DB 3; Length 4403765;  
Best Local Similarity 44.6%; Pred. No. 0.14;  
Matches 180; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 10 GCATTTGCCACACTGATTGCGCTCTCCCGCGCGCGCACTCGCGGAAGCGCATCC 69  
Db 3731458 GCGGTTGCGCGCTTGCGCGCGCGCGCGCTGCTGACGCGCGGTT 3731517  
QY 70 GCTTTTACGTCCAGCCGATGCCGACACGCAAAAGCTCAAGCTCTTAGGTTTCGC 129  
Db 3731518 GCGCGCGCGCGCGCTTGCGCGCGCGCATTCGCGGCTCCCGGACCGGC 3731577  
QY 130 AAAGGCTTCAGCCCGCGCATCTCCGAGCTACCGCATCAACGACTTCGCTTCGCGCTC 189  
Db 3731578 GTAGCGCGGTTGCGCGCGCGCGCAAAACCATCTCTGGAGAGCGCGCGCTTCGCGC 3731637  
QY 190 GATTACACGCGCTACAAAACCTATAAGCCCGCATCCACGATTTCAAACTTTACAGCATC 249  
Db 3731638 GAGCGCGCGTTGCGCGCTTAAGAAATGCGCACCGCGCTGCGCGCGCTACCGCGTT 3731697  
QY 250 GCGCGGTCGCGCATTTAGACTTCGACACCCCAATCGCCGCTCAACCGTATCTCGCGCG 309  
Db 3731698 GCGCGCTGTGCGCGCTTCGCGCGCGCATCGCGCTGCGCGCGAGCGCGCGCGCC 3731757  
QY 310 CGCTTGAGCTCAACCGCGCTCTCGCTCGACTTTGGCGCGCGAGCGAGCTTCAGCCAAAC 369  
Db 3731758 GGCACCGCGCTCCCGCGCGCGCGCGCGCAACCGCTAGCAAGTTCGCGCGC 3731817  
QY 370 TCCATCGGCTCTCGCGTATTGACGGCGTAAAGCTATGCGGTTAC 413



Qy	133	GGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAGCACTCGCTTCGCGCTCGAT	192
Db	426913	GGCATCTCGCTGACCGGGAGCGGCTTGTCCGCTTCAGCTCCGAACTCCGCGCGCGCG	426854
Qy	193	TACACGGCTACAAAACTATAAAGCCCATCCACGGATTTCAAACCTTTACAGCATCGCG	252
Db	426953	AACACCGGTTTCTTCACTTCGGCACCGGCAACACCGGCTTGTTCACTCCGGCACCGCG	426794
Qy	253	CGCTCCGCGCATTTACGACTTCGACACCCAAATCGCCCGTCAAAACCGTATCTCGCGCGCGCG	312
Db	426793	AACACCGGCTTGTTCAAATCGGGCACCGGCAACGTGGCATCGGCACATGCGGCACCGCG	426734
Qy	313	TTGAGCCTCAACCGCGCCTCCGTGCACTTGGCGCGCAGGACAGCTTCAGGCCAAACCTCC	372
Db	426733	GGCTTCGCGCGTCGGGCTATCGGGCAGCCACAGGTGGGCATCGGCGGCACCACTCGCGCG	426674
Qy	373	ATCGGCTTCGCGGTATTCACGGGCGTAAGCTATGCGCTTACCCCGAAATGTCGATTTGGAT	432
Db	426673	AGTTTCAACATCGGCTTGTTTAACTCGGGCACCGGCAATGTGGCATCGGCAACTCGGGCG	426614
Qy	433	CGCGGCTACCGCTACAACATCATCGGCAAGTCAAACACTGTCAAAAACGTCCGGTTCGCGCG	492
Db	426613	ACCGGCAACGTCCGCATCGGCAACACCGGCACCGGCAACACCGGCATCGGAACACAGCGCG	426554
Qy	493	GAACGTGTCCTCGGCGTGGCG	513
Db	426553	AACTACAACACCGGCTTGCTC	426533

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RESULT 11
US-09-881-165-4
US-09-881-165-4, Application US/09881165
; Sequence 4, Application US/09881165
; Patent No. 6632930
; GENERAL INFORMATION:
; APPLICANT: HOOD, ELIZABETH
; APPLICANT: HOWARD, JOHN
; APPLICANT: BAILLEY, MICHELE
; APPLICANT: GASTEL, FRANS VAN
; APPLICANT: WANG, HUAMING
; APPLICANT: WARD, MICHAEL
; APPLICANT: WOODARD, SUSAN
; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
; TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS
; FILE REFERENCE: 10032R
; CURRENT APPLICATION NUMBER: US/09/881,165
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/211,732
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
; OTHER INFORMATION: Organophosphate Hydrolase
US-09-881-165-4

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	Query Match	8.4%	Score 44	DB 3	Length 1082
	Best Local Similarity	46.0%	Pred. No. 0.03		
	Matches 149	Conservative 0	Mismatches 175	Indels 0	Gaps 0
Qy	31	CTCGCTCTCCGGCGCGC	CACTGGCGGAAGCGCAT	CCGGCTTTTACGTCCAAAGCCGAT	90
Db	522	CTCGTGCTCAAGGCGCG	CGCGCGCCTCCTCGCCACCGGG	GTCCGGTGACCAACCAC	581
Qy	91	GCCGCACAGCAAAAGCT	CTAAGCTCTTTAGGTTCTGCAAAAGGCT	TTCAGCCCGCGCATC	150
Db	582	ACCGCGGCTCCAGCGCG	AGCGGAGCAGCAGGCGCGCATCTTCAGAGTC	CGAGGGCCTC	641
Qy	151	TCCGGAGGCTACCGCAT	CAACGACCTCGGCTTCGGCTCGATTACACGGCT	TACAAAAC	210

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Db      642  TCCCGCTCCGGGTGTGCATCGCGCCACTCGAGCAGACACCGACGACTCTCTTACTCTCACC 2701
Qy      211  TATAAAGCCCCATCCACCGATTTCAAACTTTTACAGCATCGGCGGTGCGGCATTTAGCAC 270
Db      702  GCCCTCGCCGCGCGGGTACTACCTCATCGGCTCGACACCACTCCGCGACTCCGCCATCGGC 761
Qy      271  TTGACACCCAAATCGCCCGTCAAAACGTAATCTCGGCGCGGCTTGAGCCCTCAACCGCGCC 330
Db      762  CTGAGGAGCAACGGCTCCGGCTCGGCCCTCTCGGCATCGGCTCTCTGGCAGACCGCGGCC 821
Qy      331  TCCGTGCGATTGGCGGCGCAGCGAC 354
Db      822  CTCCTCATCAAGGCCCTCATCGAC 845

RESULT 12
US-08-961-527-363
; Sequence 363, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 363:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-363

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	Query Match	8.4%	Score 44;	DB 3;	Length 4483;
	Best Local Similarity	47.3%;	Pred. No. 0.047;		
	Matches 174;	Conservative	0;	Mismatches 185;	Indels 9; Gaps 1;
Qy	134	GCCTTCAGCCGGCGCATCTCCGCAAGGTACCGCATCAAGCACTTCGGCTTCGGCGTCGATT	193		
Db	2659	GCCTTCAGCAAGTACAGTGGCTGGCTTCAGCATCAACAGTGTCTCAGTCTCAGGTCA	2718		
Qy	194	ACACGGGCTACAAAACTATPAAAGCCCATCCACCGATTTCAAACTTTACAGCATCGGG	253		
Db	2719	ACCAGTGCCTCTGAATCAGCATCAACAAGTGCCTCGCTTCAGCAAGCACCATGTGGTGG	2778		
Qy	254	CGTCCGCGCATTTA-----CGACTTCGACACCCATCGCCCGGTCAAACCGTATCTCG	304		
Db	2779	GCCTTCAGCAAGTACTAGTGTGATCGGGCTTCAGCATCGCAAGTGGTCTGAATCGGCATCA	2838		



Qy 305 GCGCGCGCTTGAGGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCGACAGCTTCAGCC 364  
Db 2839 ACGAGTGCTTCGGCTTCAGCATCAAGGAGTGCGTCAGCCTCAGCAAGCACATCAGCTTCT 2898  
Qy 365 AAACCTCATCGGCTCGCGCTATTGACGGCGGTAAAGCTATGCGCTTACCCCGAATGTG 424  
Db 2899 GAATCTGCATCAACGAGTGCGCTTCGCTTTCAGCGCTCAACAGTGGCTTCAGCGTGG 2958  
Qy 425 ATTTGGATGCGGCTTACCGCTACCACTACATCGGCAGAAATCAACACTGTCAAAAAGTCC 484  
Db 2959 ACAAGTGCTTCGGCTTCAGCATCAAGGAGTGCGTCGGCTCAGCAAGGCGAAGTACCTCA 3018  
Qy 485 GTTCCGGC 492  
Db 3019 GCGTCAGC 3026

## RESULT 13

US-08-961-527-71  
; Sequence 71, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32768 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-527-71

Query Match 8.4%; Score 44; DB 3; Length 32768;  
Best Local Similarity 47.3%; Pred. No. 0.085;  
Matches 174; Conservative 0; Mismatches 185; Indels 9; Gaps 1;  
Qy 134 GCTTCAGCGCGGCTACCGAGGCTACCGCATCAAGCAGCTCGGCTTCGCGCTCGATT 193  
Db 1442 GTTTCAGCAAGTACCAGTGCGCTTCAGCATCAACAGTGTTCAGTCTCAGCGTCA 1501  
Qy 194 ACAGCGCTCAAAAACCTATAAGCCCATCCACGATTTCAAATTTACAGCATCGGCG 253  
Db 1502 ACCAGTGCTCTGAATCAGCATCAAAAGTGTGCTCGGCTTCAGCAGCAGCAGTGGCTG 1561  
Qy 254 GTCGCGCATTTA-----CGACTTCGACACCCAAATCGCCGTCAAAACCGTATCTCG 304

Db 1562 GCTTCAGCAAGTACTAGTGCATCGGCTTCAGCATCGCAAAAGTGTCTGAATCGGCATCA 1621  
Qy 305 GCGCGCGCTTGAGGCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCGACAGCTTCAGCC 364  
Db 1522 ACGAGTGCTTCGGCTTCAGCATCAACGAGTGCGTCAGCCTCAGCAAGCACATCAGCTTCT 1681  
Qy 365 AAACCTCATCGGCTCGGCGTATTGACGGCGGTAAAGCTATGCGCTTACCCCGAATGTG 424  
Db 1682 GAATCTGCATCAACGAGTGCGCTTCGCTTTCAGCGCTCAACAGTGGCTTCAGCGTGG 1741  
Qy 425 ATTTGGATGCGGCTACCGCTACCACTACATCGGCAGAAATCAACACTGTCAAAAAGTCC 484  
Db 1742 ACAAGTGCTTCGGCTTCAGCATCAACGAGTGCGCTTCGCGCTCAGCAAGGCGAAGTACCTCA 1801  
Qy 485 GTTCCGGC 492  
Db 1802 GCGTCAGC 1809

## RESULT 14

US-09-197-649-7  
; Sequence 7, Application US/09197649  
; Patent No. 6194550  
; GENERAL INFORMATION:  
; APPLICANT: Gold, Larry  
; APPLICANT: Tuerk, Craig  
; APPLICANT: Priebnow, David  
; APPLICANT: Smith, Jonathan D.  
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation  
; FILE REFERENCE: NEX02/CI-CON  
; CURRENT APPLICATION NUMBER: US/09/197,649  
; CURRENT FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: 07/829,461  
; EARLIER FILING DATE: 1992-01-31  
; EARLIER APPLICATION NUMBER: 07/739,055  
; EARLIER FILING DATE: 1991-08-01  
; EARLIER APPLICATION NUMBER: 07/561,968  
; EARLIER FILING DATE: 1990-08-02  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 390  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Sequence  
; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed  
; OTHER INFORMATION: fragments having NcoI restriction sites.  
US-09-197-649-7

Query Match 8.3%; Score 43.6; DB 3; Length 390;  
Best Local Similarity 45.0%; Pred. No. 0.029;  
Matches 163; Conservative 0; Mismatches 199; Indels 0; Gaps 0;  
Qy 147 CATCTCGCAGGCTACCGCATCAACGACCTTCGCTTCGCGCTCGATTACAGCGCTACAA 206  
Db 5 CATCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 64  
Qy 207 AAATATAAGCCCATTCACCGATTTCAAACTTTACAGCATCGGCGGTTCGCCATTTA 266  
Db 65 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 124  
Qy 267 CGACTTCGACACCCAAATCGCCGCTCAAAACCGTATCTCGGCGCGGCTTGAGCCTCAACCG 326  
Db 125 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 184  
Qy 327 CGCCTCGCTGACATTGGGCGGCGACGACGCTTCAGCCAAACCTCCATTCGCGCTTCGGCGT 386  
Db 185 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 244  
Qy 387 ATTGACGGGCGTAGCTATGCGGTATCCCGAATGTGATTTGGATGCGCGCTACCGCTA 446  
Db 245 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 304



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 22:10:14 ; Search time 232 Seconds  
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Title: US-10-650-123-1

Perfect score: 525

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.New.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502.6	95.7	710	7	US-11-103-957-91
2	480.2	91.5	525	6	Sequence 91, Appli
3	368	70.1	486	6	Sequence 2511, Ap
4	45.6	8.7	4617	7	Sequence 2509, Ap
5	45	8.6	9903	7	Sequence 530, App
6	44.4	8.5	687	6	Sequence 517, App
7	44.2	8.4	1659	7	Sequence 1753, Ap
8	43.8	8.3	708	6	Sequence 552, App
9	43	8.2	558	6	Sequence 2385, Ap
10	43	8.2	687	6	Sequence 7853, Ap
11	43	8.2	696	6	Sequence 6237, Ap
12	43	8.2	714	6	Sequence 5651, Ap
13	43	8.2	3990	7	Sequence 6247, Ap
14	42.8	8.2	567	6	Sequence 520, App
15	42.6	8.1	4983	7	Sequence 3183, Ap
16	41.2	7.8	843	6	Sequence 521, App
17	41.2	7.8	843	6	Sequence 7073, Ap
18	40.8	7.8	4146	7	Sequence 8005, Ap
19	40.6	7.7	834	6	Sequence 522, App
20	40.6	7.7	6210	7	Sequence 6725, Ap
21	40.4	7.7	681	6	Sequence 1, Appli
22	40.4	7.7	681	6	Sequence 53, Appli
23	40.4	7.7	795	6	Sequence 829, App
					Sequence 1777, Ap

24	40.4	7.7	834	6	US-10-467-657-7385	Sequence 7385, Ap
25	40.4	7.7	939	6	US-10-467-657-7399	Sequence 7399, Ap
26	40.4	7.7	3711	6	US-10-873-528-321	Sequence 321, App
27	39.4	7.5	5706	7	US-11-052-554A-519	Sequence 519, App
28	39.2	7.5	2562	7	US-11-052-554A-533	Sequence 533, App
29	39	7.4	1280	6	US-10-802-796-4	Sequence 4, Appli
30	39	7.4	2406	7	US-11-052-554A-550	Sequence 550, App
31	39	7.4	89421	7	US-11-205-109-1	Sequence 1, Appli
32	38.8	7.4	1650	6	US-10-858-730-140	Sequence 140, App
33	38.4	7.3	5706	7	US-11-052-554A-519	Sequence 519, App
34	38.2	7.3	678	6	US-10-467-657-6037	Sequence 6037, Ap
35	38.2	7.3	1632	7	US-11-052-554A-546	Sequence 546, App
36	38.2	7.3	3240	7	US-11-052-554A-529	Sequence 529, App
37	38	7.2	2196	7	US-10-467-657-2721	Sequence 539, App
38	38	7.2	2277	6	US-11-052-554A-539	Sequence 2721, Ap
39	38	7.2	6615	7	US-11-052-554A-518	Sequence 518, App
40	37.2	7.1	888	6	US-10-858-730-183	Sequence 183, App
41	37.2	7.1	1497	6	US-10-467-657-2095	Sequence 2095, Ap
42	37.2	7.1	1821	7	US-11-052-554A-547	Sequence 547, App
43	36.6	7.0	2205	6	US-10-467-657-3729	Sequence 3729, Ap
44	36.6	7.0	2205	6	US-10-467-657-6989	Sequence 6989, Ap
45	36.6	7.0	2337	7	US-11-052-554A-528	Sequence 528, App

#### ALIGNMENTS

#### RESULT 1

US-11-103-957-91  
; Sequence 91, Application US/11103957  
; Publication No. US20050281847A1  
; GENERAL INFORMATION:  
; APPLICANT: Berthet, Francois-Xavier Jacques  
; APPLICANT: Lobet, Yves  
; APPLICANT: Poolman, Jan  
; APPLICANT: Verlant, Vincent Georges Christian Louis  
; TITLE OF INVENTION: Vaccine Composition  
; FILE REFERENCE: B45261  
; CURRENT APPLICATION NUMBER: US/11/103,957  
; CURRENT FILING DATE: 2005-04-12  
; PRIOR APPLICATION NUMBER: US/10/467,534  
; PRIOR FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: PCT/EP02/01356  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: GB 0103169.9  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 710  
; TYPE: DNA  
; ORGANISM: Neisseria gonorrhoeae

Query Match 95.7%; Score 502.6; DB 7; Length 710;  
Best Local Similarity 97.3%; Pred. NO. 2.1e-125;  
Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy	1	ATGAAAAAGCATTGCCACACTGATTCGCTCTCCGCGCGCGCGCGCGGAA	60
Db	141	ATGAAAAAGCATTGCCACACTGATTCGCTCTCCGCGCGCGCGCGCGGAA	200
Qy	61	GGCGCATCCGCTTTTACGTCCAAAGCCGATGCCGACACGCAAAAGCTCTTCTT	120
Db	201	GGCGCATCCGCTTTTACGTCCAAAGCCGATGCCGACACGCAAAAGCTCTTCTT	260
Qy	121	GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC	180
Db	261	GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC	320
Qy	181	TTCCCGCTCGATTACACCGGCTACAAAACCTATAAAGCCCATCCACCGATTTCAACTT	240
Db	321	TTCCCGCTCGATTACACCGGCTACAAAACCTATAAAGCCCATCCACCGATTTCAACTT	380

Qy 241 TACAGCATCGCGGCTCGCCATTTACGACTTTCGACACCCCAATCGCCGTCGCTCAAAACCGTAT 300  
Db 381 TACAGCATCGCGGCTCGCTCATTTACGACTTTCGACACCCCAATCGCCGTCGCTCAAAACCGTAT 440  
Qy 301 CTCGGCGCGCTTGAGCTCAACCGCGCTCGCTCGACTTCGCTGCGGCGGCGAGCGACGCTTC 360  
Db 441 TTCGGCGCGCTTGAGCTCAACCGCGCTTCGCGCCACTTCGCGCGGCGAGCGACGCTTC 500  
Qy 361 AGCCAAACCTCCATCGGCTCGGCGTATTTGACGGGCTAAGCTATGCGTTACCCCGAAT 420  
Db 501 AGCAAAACCTTCGCGGCTCGCGGTATTTGCGGCGGCTAAGCTATGCGTTACCCCGAAT 560  
Qy 421 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480  
Db 561 GTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAAC 620  
Qy 481 GTCGCTTCGCGCAACTGCTCGTGGCGTGGCGTGGCGTCAAAATTCGA 525  
Db 621 GTCGCTTCGCGCAACTGCTCGGCGGCTGGCGTGGCGTCAAAATTCGA 665

RESULT\*2  
US-10-467-657-2511  
; Sequence 2511, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2511  
; LENGTH: 525  
; TYPE: DNA  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2511

Query Match 91.5%; Score 480.2; DB 6; Length 525;  
Best Local Similarity 96.0%; Pred. No. 2e-119;  
Matches 504; Conservative 0; Mismatches 18; Indels 3; Gaps 1;  
Qy 1 ATGAAAAAGCACTTGCCACACTGATTCGCTCTCCGCGCGCGCACTGCGGAA 60  
Db 1 ATGAAAAAGCACTTGCCGCACTGATTCGCTCTCCGCGCGCGCACTGCGGAA 60  
Qy 61 GCGCATCCGCTTTTACGTCGCAAGCGGATGCGGACACGCAAGCAAGCTCAAGCTCTTTA 120  
Db 61 GCGCATCCGCTTTTACGTCGCAAGCGGATGCGGACACGCAAGCTCAAGCTCTTTA 120  
Qy 121 GGTTCGCAAAAGGCTTACGCGCGGCTACCGGAGGCTACCGATCAACGACTTCGC 180  
Db 121 GGTTCGCAAAAGGCTTACGCGCGGCTACCGGAGGCTACCGATCAACGACTTCGC 180  
Qy 181 TTGCGGTCGATTAACGCGCTACAAAACCTATATAACGAGCCCATCCACGATTTCAA 237  
Db 181 TTGCGGTCGATTAACGCGCTACAAAACCTATATAACGAGCCCATCCACGATTTCAA 240  
Qy 238 CTTTACAGCATCGGCGCTCGCCATTTACGACTTTCGACACCCCAATCGCCGTCGCAACCG 297  
Db 241 CTTTACAGCATCGGCGCTCGCTCATTTACGACTTCGACACCCCAATCGCCGTCGCAACCG 300  
Qy 298 TATCTCGCGCGCTTTCGAGCTCAACCGCGCTCCGCTGACTTGGGCGGCGAGCGACG 357  
Db 301 TATTTGCGCGCGCTTTCGAGCTCAACCGCGCTTCGCGCCACTTGGGCGGCGAGCGACG 360

Qy 358 TTCAGCCAAACCTCCATCGGCTCGGCTATTTGACGGGCGTAAAGCTATGCGTTACCCCG 417  
Db 361 TTCAGCAAAACCTCCCGCGCTCGGGGTATTTGGCGGGCGTAAAGCTATGCGTTACACCC 420  
Qy 418 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 477  
Db 421 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 480  
Qy 478 AAGTTCGCTTCGCGCAACTGCTCGTGGGCTGGCGTCAAAATTC 522  
Db 481 AAGTTCGCTTCGCGCAACTGCTCGCGGCGTGGCGTCAAAATTC 525

RESULT 3  
US-10-467-657-2509/c  
; Sequence 2509, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2509  
; LENGTH: 486  
; TYPE: DNA  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2509

Query Match 70.1%; Score 368; DB 6; Length 486;  
Best Local Similarity 95.6%; Pred. No. 2.1e-89;  
Matches 390; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
Qy 121 GGTTCGCAAAAGGCTTACGCGCGGCTACCGCGCATCTCGCAGGCTACCGCATCAACGACTTCGC 180  
Db 486 GGTTCGCAAAAGGCTTACGCGCGGCTACCGCGCATCTCGCAGGCTACCGCATCAACGACTTCGC 427  
Qy 181 TTGCGGTCGATTAACGCGCTACAAAACCTATAAACAAGCCCATCCACGATTTCAA 237  
Db 426 TTGCGGTCGATTAACGCGCTACAAAACCTATAAACAAGCCCATCCACGATTTCAA 367  
Qy 238 CTTTACAGCATCGGCGCTCGCCATTTACGACTTTCGACACCCCAATCGCCGTCGCAACCG 297  
Db 366 CTTTACAGCATCGGCGCTCGCTCATTTACGACTTTCGACACCCCAATCGCCGTCGCAACCG 307  
Qy 298 TATCTCGCGCGCTTTCGAGCTCAACCGCGCTTCGCTGAGCTTGGGCGGCGAGCGACG 357  
Db 306 TATTTGCGCGCGCTTTCGAGCTCAACCGCGCTTCGCGCCACTTGGGCGGCGAGCGACG 247  
Qy 358 TTGAGCAAAACCTCCATCGGCTCGGCTATTTGACGGGCTAAGCTATGCGTTACCCCG 417  
Db 246 TTGAGCAAAACCTCCCGCGCTCGGCTATTTGGCGGGCGTAAAGCTATGCGTTACACCC 187  
Qy 418 AATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAA 477  
Db 186 AATGTCGATTTGGATGCGGCTACCGCTACAACTACGTCGCGCAAAAGTCAACACTGTCAA 127  
Qy 478 AAGTTCGCTTCGCGCAACTGCTCGTGGGCTGGCGTCAAAATTCGA 525  
Db 126 AAGTTCGCTTCGCGCAACTGCTCGCGGGCGTGGCGTCAAAATTCGA 79

RESULT 4  
US-11-052-554A-530/c



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Query Match      8.2%; Score 43; DB 6; Length 558;
Best Local Similarity 69.9%; Pred. No. 0.021;
Matches 59; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy      248  TCGCGCGTCCGCCATTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTATCTCGCGC 307
        |||||
Db      191  TCGGCTTGTCCGCGGTTTACGATTTCGATACCGGTTCCCGCTTCAAAACCTATGACAGCG 250
        |||||

Qy      308  CGCGCTTGAGCCTCAACCGCGCC 330
        |||||
Db      251  TCGCGCTCAGCTACGGACAGTC 273
        |||||

RESULT 10
US-10-467-657-6237
; Sequence 6237, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita

```







GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 19:58:14 ; Search time 3281 Seconds  
(without alignments)  
7486.504 Million cell updates/sec

Title: US-10-650-123-1  
Perfect score: 525  
Sequence: 1 atgaaaaagcacttgccac.....gcgtgcgcgtcaaatctga 525

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57.8	11.0	622	6	CA197724 SCAGAD107
2	56.4	10.7	626	6	CA193415 SCCFL100
3	55.2	10.5	787	6	CB654660 OSJNEC07F
4	54.2	10.3	743	10	C2247380 AIAA-aaf3
5	53.6	10.2	591	6	CB640993 OSJNEal7F
6	53.6	10.2	665	7	CV152413 LS245-S.S
7	53.6	10.2	698	6	CB653730 OSJNEC05A
8	53.6	10.2	725	6	CB677411 OSJNEal4E
9	53.6	10.2	741	6	CF589226 EST00F06
10	53.6	10.2	759	6	CB671800 OSJNEe05I
11	53.6	10.2	762	6	CB677339 OSJNEal4C
12	53.6	10.2	775	6	CB677062 OSJNEal3K
13	53.6	10.2	778	6	CB654692 OSJNEC07G
14	53.6	10.2	782	6	CB665147 OSJNEd11F
15	53.6	10.2	842	6	CB668023 OSJNEd15K
16	53.4	10.2	561	6	CF278525 14ETL--04
17	53.4	10.2	644	6	CF315326 HD--04-D0
18	52.2	9.9	525	6	CF308604 ABF--02-H
19	52	9.9	696	6	CD935542 OV.101M15
20	51.8	9.9	530	6	CF335206 JMT--04-M
21	51.8	9.9	558	2	BG560231 RH122_71
22	51.8	9.9	655	6	CA172233 SCSPFB107

## ALIGNMENTS

RESULT 1  
CAL197724  
LOCUS SCAGAD1074C04.g AD1 Saccharum officinarum cDNA clone SCAGAD1074C04  
DEFINITION 5', mRNA sequence.  
ACCESSION CAL197724  
VERSION CAL197724.1 GI:35228269  
KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.

REFERENCE 1 (bases 1 to 622)  
Vettore,A.L., da Silva,P.R., Kemper,B.L. and Arruda,P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parvada@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccnet.fca.vunesp.br  
Plate: 074 row: C column: 04  
Seq primer: T7 Promoter Primer.

FEATURES  
Location/Qualifiers  
1..622  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCAGAD1074C04"  
/lab\_host="DH10B"  
/clone\_lib="AD1"  
/note="Organ: seedlings inoculated with Gluconacetobacter  
diazotrophicans; Vector: pSport1; Site 1: SalI; Site 2:  
NotI; An unidirectional cDNA library generated from  
[seedlings inoculated with Gluconacetobacter  
diazotrophicans]. cDNA was prepared from polyA+ mRNA using  
Superscript Plasmid System Kit (Invitrogen). The  
double-strand cDNAs were fractionated in a sepharose

CA253038 SCJPL409  
CA231223 SCQSL303  
DN655133 CEC15-C02  
CV097296 FAMU USDA  
BH898151 MB61P2A7  
CD219573 CCC1\_57\_A  
CD222538 CCC1\_22\_G  
CD222866 CCC1\_24\_B  
CB681064 OSJNEI06N  
CL978445 OsIFCC031  
CL973983 OsIFCC025  
BJ748832 BJ748832  
CL971648 OsIFCC021  
CB643751 OSJNEB04J  
BK167632 FGAS05203  
BG560157 RH122\_71  
AI389106 GH20192\_5  
CD223038 CCC1\_25\_B  
AM680997 WS1\_9\_E10  
BE593027 WS1\_93\_D1  
BE357605 DGI\_21\_E0  
CD463595 ETH1\_45\_P  
CW197767 104\_622\_1

CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

## ORIGIN

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Query Match      11.0%; Score 57.8; DB 6; Length 622;
Best Local Similarity 47.4%; Pred. No. 5.3e-05;
Matches 173; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 27 TGCCTCGCTCTCCGCGCGCGGCACTGGCGGAAGGCGCATCCGGCTTTACGTCCAGC 86
Db 108 TGATCGCTCTCGGCGATCGCATATTCACCGCGGCGCATCCCGGTGACGCGAAG 167
Qy 87 CGATGCGCGCACACGCAAAAGCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCGCG 146
Db 168 CGCCACGCTCGAATCTCCCGCGCCACGCGGCGCGGCGCTCAGGCGCTCCAGAGGCA 227
Qy 147 CATCTCGCGAGGTACCGCATCAACGACCTCCGCTTGCGCGTGCATTACAGCGCTACAA 206
Db 228 ACCGCTCTCCGCGCCACGCGCACTCTCCCGCGCTCCGAGCAGCAGCGCGCCCGCG 287
Qy 207 AAATATTAAGCCCGATCCACGATTTCAAACTTTACAGCATCGCGGCTCCGCAATTA 266
Db 288 CACCACCGACACAGCTTTCTCGGCTCCCAACAGCGCGTCCCGCGCGCGCGCACTC 347
Qy 267 CGACTTGCACACCAATCGCCGTCMAACCGTATCTCGGCGCGGCTTGAGCTCAACCG 326
Db 348 CTTCTCCAGCGCCACACGCGCTCTCGTCAACGTCGCGGAGCGCGCTACCGGTTCCA 407
Qy 327 CGCTTCGCTGACTTGGCGCGCAGCGAGCTTCAGCCAAACCTCCATCGCGCTCGGCT 386
Db 408 CCACTCGCTGCGCTCTCCCGCGGTGAGCGCGACACCGCGTCCCGCGCACCTTGGCGT 467
Qy 387 ATTGA 391
Db 468 TTCA 472

```

## RESULT 2

```

CA193415
LOCUS          626 bp mRNA linear EST 24-SEP-2003
DEFINITION    SCCEFL1003E05.g FL1 Saccharum officinarum cDNA clone SCCEFL1003E05
              5', mRNA sequence.

```

CA193415

CA193415.1 GI:35140555

EST.

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

## REFERENCE

1 (bases 1 to 626)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: [parruda@unicamp.br](mailto:parruda@unicamp.br)

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: 003 row: E column: 05

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..626

/organism="Saccharum officinarum"

/mol\_type="mRNA"

## FEATURES

source

/db\_xref="taxon:4547"  
/clone="SCCEFL1003E05"  
/lab\_host="DH10B"  
/clone\_lib="FL1"

/note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSport1; Site\_1: SalI; Site\_2: NotI; An unidirectional cDNA library generated from (Inflorescence at beginning of development (1cm-long)). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

## ORIGIN

```

Query Match      10.7%; Score 56.4; DB 6; Length 626;
Best Local Similarity 47.2%; Pred. No. 0.00013;
Matches 171; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Qy 27 TGCCTCGCTCTCCGCGCGCGGCACTGGCGGAAGGCGCATCCGGCTTTACGTCCAGC 86
Db 58 TGATCGCTCTCGGCGATCGCATATTCACCGCGGCGCATCCCGGTGACGCGAAG 117
Qy 87 CGATGCGCGCACACGCAAAAGCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCGCG 146
Db 118 CGCCACGCTCGAATCTCCCGCGCCACGCGGCGCGGCTCAGGCGCTCCAGAGGCA 177
Qy 147 CATCTCGCGAGGTACCGCATCAACGACCTTCGCGTTCGCGTGCATTACAGCGCTACAA 206
Db 178 ACCGCTCTCCGCGCCACGCGCACTCTCCCGCGGTCCGAGCAGCAGCGCGCCCGG 237
Qy 207 AAATATTAAGCCCGATCCACGAGCTTCAGCAACTTTACAGCATCGCGCGCTTGAGCTCA 266
Db 238 CACCACCGACACGCTCTCCGCTCCCAACGCGCGCGCGCGCGCGCGCGCGCACTC 297
Qy 267 CGACTTGCACACCAATCGCGCGCTCAACCGCTATCTCGGCGCGGCTTGAGCTTCAGCCG 326
Db 298 CTCTCCAGCGCGCCACACGCGCTCCGTCACGCGCGCGGAGCGCGCGCGCTCCCA 357
Qy 327 CGCTTCGCTGACTTGGCGCGCAGCGAGCTTCAGCCAAACCTCCATCGCGCTCGGCT 386
Db 358 CCACTCGCGCGCTCTCCCGCGGTGAGCGCGACACCGCGTCCCGCGCACCTTGGCGT 417
Qy 387 AT 388
Db 418 CT 419

```

## RESULT 3

CB654660

LOCUS

DEFINITION

OSJNEC07F21.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA

clone OSJNEC07F21 5', mRNA sequence.

CB654660

ACCESSION

VERSION

CB654660.1 GI:29658385

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 787)

Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,

Shahbarg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,

Soderlund,C. and Wang,G.L.

Large-scale identification of expressed sequence tags involved in

rice and rice blast fungus interaction

Plant Physiol. 138 (1), 105-115 (2005)

15886883

PUBMED

COMMENT

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona  
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
 85721-0088, USA  
 Tel: 520 626 3967  
 Fax: 520 621 9288  
 Email: rwing@genome.arizona.edu  
 PCR Primers  
 FORWARD: gta aaa cga cgg cca gtcg  
 BACKWARD: gga aac agc tat gac cat g  
 Plate: 07 row: F column: 21  
 Seq primer: gta aaa cga cgg cca gtcg.

FEATURES  
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 /organism="Oryza sativa (japonica cultivar-group)"  
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 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone="OSJNEC07P21"  
 /tissue\_type="Leaf"  
 /dev\_stage="3 week"  
 /lab\_host="DH10B"  
 /clone\_lib="OSJNEC"  
 /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"  
 ORIGIN  
 Query Match 10.5%; Score 55.2; DB 6; Length 787;  
 Best Local Similarity 44.7%; Pred. No. 0.00029;  
 Matches 213; Conservative 0; Mismatches 263; Indels 0; Gaps 0;

QY 41 CGGCCGCGCACTGCGGAGCGGATCGGCTTTTACGTCGCAAGCGGATGCGGACAG 100  
 Db 60 CAGCAGCGCCATGAGGAGATACGACCGCGAGTCTTACGAGTTCCCGACGAGCTCGCGC 119  
 QY 101 CAAGAAGCTCAGCTCTTAGGTTCTGCAAGAGCTTCAGCGCGCATCTCGCGAGGT 160  
 Db 120 TGCAGAGCGCGAGCTCTCCGCGCTCTCCCTCGCGAGCTCCATCTGCTCTCCCTCG 179  
 QY 161 ACCGCGATCAAGCACTCGGCTTCGCGCTGATTCACGCGGCTACAAAACATATAAGGCC 220  
 Db 180 ACCGCGGCAACGAGCGGCTTCGAGCGGAGTACACCACTTCTCTCCCTCCCGCG 239  
 QY 221 CATCACCGATTTCAAACTTTACAGATCGCGCGCTCGCGCATTTACGATTCGACACCC 280  
 Db 240 CCAAGAACGCCATCGCCCAACATCAACGCGCTCGCGGAACTCTGATGCGCGCGCTCA 299  
 QY 281 AATCGCGCTCAACCGTATCTCGGCGCGGCTTGAGCTCAACCGCGCTCGGCTCGACT 340  
 Db 300 TGGGCTCGGCAAGCTCGGCTTCGCGCGCAACGCGCGGAGCGCTTACACAGCGTCAACC 359  
 QY 341 TGGGCGGAGGACAGCTTCAGCCAAACCTCCATCGGCTCGGCGTATTTGAGCGGCGTAA 400  
 Db 360 TCCCGCTGCAACAAACAAACAAACAGTCTTACGCGGCGCGCGCGAGATCAACACA 419  
 QY 401 GCTATCGCGTTACCCGGAATGATTTGATTTGATTCGCGGCTTACCGCTTACATATCGGCA 460  
 Db 420 ACAAGTCAACGCTTCGGGTTCAACAGATGCGGCGTTTACAAACAGCAGCAGCAACGGCG 479  
 QY 461 AGTCAACACTGTCAAAACGTCGCTTCGCGGCAACTGCTCGGCGGCTCGGCGTTC 516  
 Db 480 GCGGCAACTACGCGGCGCAACGCGCGGAGCTGTAAGAGCTACTTCAACAGTCTCGGTC 535

RESULT 4  
 C2247380  
 LOCUS  
 DEFINITION  
 A1AA-aaf35a12.b1 Ancylostoma caninum whole genome shotgun library (A1AAGSS 001)  
 ACCESSION  
 C2247380  
 VERSION  
 C2247380.1  
 KEYWORDS  
 GSS.  
 SOURCE  
 Ancylostoma caninum (dog hookworm)  
 ORGANISM  
 Ancylostoma caninum

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma. 1 (bases 1 to 743)  
 Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R., Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D., Waterston,R.H., Clifton,S.W. and Wilson,R.  
 Genome Survey sequences from the parasitic nematode Ancylostoma caninum  
 Unpublished (2004)  
 Contact: Mitreva M  
 Washington University in St. Louis  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: nematode@watson.wustl.edu  
 Genomic DNA provided by John Hawdon (mtmjmh@wumc.edu) DNA sequenced by Washington University Genome Sequencing Center  
 Class: shotgun.

FEATURES  
 source  
 1..743  
 /organism="Ancylostoma caninum"  
 /mol\_type="genomic DNA"  
 /strain="Baltimore"  
 /db\_xref="taxon:29170"  
 /dev\_stage="Adult"  
 /lab\_host="GS10"  
 /clone\_lib="Ancylostoma caninum whole genome shotgun library (A1AAGSS 001)"  
 /note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI; Ancylostoma caninum genomic DNA was randomly sheared, end-repaired and size fractionated to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmjmh@wumc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."

ORIGIN  
 Query Match 10.3%; Score 54.2; DB 10; Length 743;  
 Best Local Similarity 47.0%; Pred. No. 0.00054;  
 Matches 167; Conservative 0; Mismatches 188; Indels 0; Gaps 0;  
 QY 129 CAAGGCTTCAGCGCGCGATCTCGCAGGCTACCGATCAACGACCTCCGCTTCGCGT 188  
 Db 113 CAACAAACGACAAACAAACGACGACAAACGACAAACGACAAACGACAAACGACAA 172  
 QY 189 CGATTACAGCGCTACAAAATATAGAGCCCATCCACCGATTTCAAACTTTACAGCAT 248  
 Db 173 CAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 232  
 QY 249 CGGCGCGTCCGCGCATTTACGACTTCGACACCAATCGCGCGTATCTCGGCGC 308  
 Db 233 CAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 292  
 QY 309 GCGCTTGAGCTCAACCGCGCTCGTTCGACTTTGGGCGGCGGAGCGAGCTTCAGCGCAAC 368  
 Db 293 CAACGACAAACAAACAAACGACGACGACGACGACGACGACGACGACGACGACGAC 352  
 QY 369 CTCCATCGGCTCGCGCTATTGAGCGGCGTAAAGCTATGCGCTTACCCCGAGTGTGATT 428  
 Db 353 CAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 412  
 QY 429 GGATCGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAACGTC 483  
 Db 413 CAACGACAAACAAACGACGACGACGACGACGACGACGACGACGACGACGACGAC 467

RESULT 5  
 C2247380  
 LOCUS  
 DEFINITION  
 OSJNEal7P21.f OSJNEa Oryza sativa (japonica cultivar-group) CDNA clone OSJNEal7P21 5', mRNA sequence.  
 ACCESSION  
 C2247380

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VERSION CB640993.1 GI:29635984
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 591)
REFERENCE Jantaauriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
AUTHORS Stahlberg,B., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 1588683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: atc agc ggc cgc gat cc
BACKWARD: aat taa ccc tca cta aag gg
Plate: 17 row: F column: 21
Seq primer: atc agc ggc cgc gat cc.
FEATURES
source
1..591
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSUNBA17F21"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSUNBA"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after inoculation with Rice Blast (Che
86061)"
ORIGIN
Query Match 10.2%; Score 53.6; DB 6; Length 591;
Best Local Similarity 44.5%; Pred. No. 0.00077;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
Qy 41 CGGCGCGGCACTGGCGGAAGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGACAG 100
Db 36 CAGCAGCGGCATGGAGGGATACACCGCGAGTTCTACCACTTCAGCGACAGCTGGCG 95
Qy 101 CAAAAGCCTCAAGCTCTTAGGTTCTGCAAGGCTTCAGCCCGCATCTCCGAGGCT 160
Db 96 TGCAGACGGCGAGCTTCTCGGCGCTCTCCCTCGCGACTTCATCTGGTCTCTCCCTCG 155
Qy 161 ACCGATCAAGCACTCGCTTCGCTCGCTGATTACCGGTACAAAACATATAAGCCC 220
Db 156 ACCGCGCAAGCGCGGCTTCGACGGCGAGTACCACTTCTCTCCCTCCCTCCCG 215
Qy 221 CATCCACGATTTCAAACTTTACAGCATCGGCGGTTCGCCATTTAGACTTCGACACCC 280
Db 216 CCAAGACGCATCGCCAACTCAACGGGTGCGCGGAACTGATGGCCCGGCTCA 275
Qy 281 AATCGCCGTCAAACCGTATCTCGCGCGCGCTTTAGCGCTCAACGGCGCTTCGCTGACT 340
Db 276 TCGGCTCGGCAAGCTCGCTTCGCGCGCACCAAGCGCGAGCTTACAAAGCGTCAACC 335
Qy 341 TGGGCGGCGAGCAGCTTCAGCCAAACCTCCATCGGCTCGGCTTATGACGGCGTAA 400
Db 336 TCCCGCTCGAACAACAACAACAACAAGTCTTACGGCGGCGCGCCAAAGATCAACA 395
Qy 401 GCTATGCGGTTACCCCGAATGTGATTTGGATGGCGGTACCGCTACAACTACATCGGCA 460
396 ACAACGTCAACGCTTCGGGTTCACCAAGATGGGGGTTCACCAACAGCAGCAACGCGC 455
461 AAGTCAACACTGTCAAAAAGCTTCGGTTCGGCGAGACTGTTCGGTGGCGGTGCGCTC 516
456 GCGCAACTAGCGGCGCAACGCGGCGGCGAGCTGAAGAGCTACTTCAACAAAGTCGCTC 511
RESULT 6
CV152413 665 bp mRNA linear EST 08-SEP-2004
LOCUS LS245-S.SEQ Cold stressed rice cDNA library Oryza sativa (japonica
DEFINITION cultivar-group) cDNA, mRNA sequence.
ACCESSION CV152413
VERSION CV152413.1 GI:51946072
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 665)
REFERENCE Lee,J.-S.
AUTHORS Isolation and chromosomal mapping of the rice clones differentially
TITLE induced under abiotic stress conditions
JOURNAL Unpublished (2004)
COMMENT Contact: Lee Jung-Sook
Bioinformatics Team
National Institute of Agricultural Biotechnology, Rural Development
Administration
225 Seodundon, Suwon, 441-707, Korea
Tel: 82 31 299 1663
Fax: 82 31 299 1722
Email: junglee@da.go.kr.
FEATURES
source
1..665
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Ilpumbyeon"
/db_xref="taxon:39947"
/tissue_type="Leaf"
/dev_stage="one week old"
/clone_lib="Cold stressed rice cDNA library"
/notes="Vector: pBluescript SK+; Cold treatment by placing
at 40C for 16 hour after growth on MS medium for one week"
ORIGIN
Query Match 10.2%; Score 53.6; DB 7; Length 665;
Best Local Similarity 44.5%; Pred. No. 0.00078;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
Qy 41 CGGCGCGGCACTGGCGGAAGCGCATCCGGCTTTTACGTCCAAGCGATGCCGACAG 100
Db 46 CAGCAGCGGCATGGAGGGATACACCGCGAGTTCTACCACTTCAGCGACAGCTGGCG 105
Qy 101 CAAAAGCCTCAAGCTCTTTAGTTCGCAAGGCTTCAGCCCGCATCTCCGAGGCT 160
Db 106 TGCAGACGGCGAGTTCTCGGCTCTCTCCCTCGCGACTTCATCTGCTCTCCCTCG 165
Qy 161 ACCGATCAACGAGCTTCGCTTCGCTGCGATTACAGCGGTACAAAACATATAAGCCC 220
Db 166 ACCGCGCAACGAGCGGCTTCGACGGCGAGTACCACTTCTCTCCCTCCCTCCCG 225
Qy 221 CATCCACGATTTCAAACTTTACAGCATCGGCGGTTCGCCATTTAGACTTCGACACCC 280
Db 226 CCAAGAACGCATCGCCAACTCAACGGCGTTCGCGGAACTCGATGGCCCGGCTCA 285
Qy 281 AATCGCCGTCAAACCGTATCTCGGCGCGCGCTTTAGCGCTCAACGGCGCTTCGCTGACT 340
Db 286 TCGGCTCGGCAAGCTCGCTTCGCGCGCACCAAGCGCGAGCTTACAAAGCGTCAACC 345
Qy 341 TGGGCGGCGAGCAGCTTCAGCCAAACCTTCATCGGCTCGGCTTATGACGGCGTAA 400
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Db 346 TCCCGTCGACAAACAACAACAAGTCTACGGCGGCGCCCAAGATCAACAACA 405

Qy 401 GCTATGCGGTATACCCGGAATGCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCA 460

Db 406 ACAAGTCAACGCGCTTCGGGTTCAACAAGATGGGGGTTACAACAACAGCAGCAGCGGG 465

Qy 461 AAGTCAACACTGTCAAAAACGTCGCTTCGGGGGAACGTGCTCGTGGCGTGCGCGTC 516

Db 466 GCGGCAACTACGGCGGCAACGCGCGAGCTGTAAGAGCTACTTCAACAAGTGGGTC 521

RESULT 7

CB653730

LOCUS OSJNEC05A17.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA

DEFINITION clone OSJNEC05A17 5', mRNA sequence.

ACCESSION CB653730

VERSION CB653730.1 GI:29657455

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 698)

AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G., Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A., Soderlund,C. and Wang,G.L.

TITLE Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction

JOURNAL Plant Physiol. 138 (1), 105-115 (2005)

PUBMED 1588683

COMMENT Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aaa cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 05 row: A column: 17

Seq primer: gta aaa cga cgg cca gtc.

FEATURES

Location/Qualifiers

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/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="OSJNEC05A17"

/tissue\_type="Leaf"

/dev\_stage="3 week"

/lab\_host="DH10B"

/clone\_lib="OSJNEC"

/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Query Match 10.2%; Score 53.6; DB 6; Length 698;

Best Local Similarity 44.5%; Pred. No. 0.00079;

Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCATCGCGGAAGCGCATCGGGCTTTTACGTCCAAAGCGCATCGCGGACAGG 100

Db 47 CAGCAGCGGCATGAGGAGATACGACCGCGAGTTCTACAGTCCCGCGCAGCATCGCGC 106

Qy 101 CAAGAGCCTCAAGCTCTTTAGGTCTGCCAAGAGCTTCAGCGCGCATCTCGCGAGGCT 160

Db 107 TGCAGAGCGGAGCTTCTCCGCGCTCTCTCCGCGCATCTTCATCTGCTCTCCCTCCG 166

Qy 161 ACCGATCAACGACCTCGCTTCGCGCTGATTTACACGCGCTACAAAGCTATAAGGCC 220

Db 167 ACCGCGCAACGAGCGGCGCTTCGACGCGGAGTACCACTTCTCTCCCTCCCGG 226

Qy 221 CATCACCGATTTCAAACCTTTACAGCATCGCGGCTCGCCATTTTACGACTTCGACACCC 280

Db 227 CCAAGACGCCATCGCAACATCAACGCGCTCGCGGAAACCTGGATGCGCGGCGCTCA 286

Qy 281 AATCGCGCTCAACCGTATCTCGCGCGCGCTTGAGCTCAACGCGCGCTTCGCTGACT 340

Db 287 TCGGCTCGGCAAGCTCGCTTCGCGCGCCACAGGCGGACGCTTACAAACAGCGCTCAACC 346

Qy 341 TGGGCGGACGACAGCTTCAGCCAAACCTCCATCGGCTCGGCTATTTAGCGGCGTAA 400

Db 347 TCCCGCTGCAACAACAACAACAACAGTCTTACGCGGCGCCGCCAAGATCAACAACA 406

Qy 401 GCTATGCGCTTACCCCGGAATGTGATTTGGATGCGCGCTACCGCTTACAACTACATCGGCA 460

Db 407 ACAAGCTCAACGCTTCGGGTTCAACAGATGGGGGTTACAACAACAGCAGCAACGGCG 466

Qy 461 AAGTCAACACTGTCAAAAACGTCGCTTCGCGGGAACGTGCTCGTGGCGTGCGGTC 516

Db 467 GCGGCAACTACGGCGGCAACGCGCGAGCTGTAAGAGCTACTTCAACAAGTGGTC 522

RESULT 8

CB677411

LOCUS OSJNE14E24.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA

DEFINITION clone OSJNE14E24 5', mRNA sequence.

ACCESSION CB677411

VERSION CB677411.1 GI:29681136

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 725)

AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G., Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A., Soderlund,C. and Wang,G.L.

TITLE Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction

JOURNAL Plant Physiol. 138 (1), 105-115 (2005)

PUBMED 1588683

COMMENT Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aaa cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 14 row: E column: 24

Seq primer: gta aaa cga cgg cca gtc.

FEATURES

Location/Qualifiers

1..725

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="OSJNE14E24"

/tissue\_type="Leaf"

/dev\_stage="3 week"

/lab\_host="DH10B"

/clone\_lib="OSJNEC"

/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN

Query Match 10.2%; Score 53.6; DB 6; Length 725;  
Best Local Similarity 44.5%; Pred. No. 0.00079;  
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCGACTGGCGAAGCGCATCGCGCTTTTACGTCAAGCCGATCGCGCACAG 100  
Db 22 CAGCAGCGCGCATGGAGGGATACGACCGCGAGTTCTACCAAGTTTCAGCGACAGCTGCGGC 81

Qy 101 CAAAAGCCTCAAGCTCTTTAGTCTTGCCAAAGGCTTCAGCGCGGCATCTCCCGCAGGCT 160  
Db 82 TGCAGACGGCGAGCTTCTCGGCGCTCTCCCTCGGGGACTCCATCTGGTCTCTCCGCTCG 141

Qy 161 ACCGATCAACGACCTCCGCTTCGCGCTGCGATACACGCGTACAAAACTATAAAGCCC 220  
Db 142 ACCGCGCAACGAGCGCGCTTCGACGCGGAGTACCACTTCTCTCCCTCCGCTCCGCG 201

Qy 221 CATCCACGATTTCAAACTTTACAGCATCGGCGGCTCGGCATTTACAGCTTCGACACCC 280  
Db 202 CCAAGACGCCATCGCCAAACATCAACGCGCTCGCGGAACTCGATGGCCCGGCGCTCA 261

Qy 281 AATCGCGCTCAACCGTATCTCGGCGCGCTTGAGCCTCAACGCGCGCTCCGCTCGACT 340  
Db 262 TCGGCTCGGCAAGCTCGCTTCGCGCGCACCAAGCGCGACGCTACCAAGCGCTCAACC 321

Qy 341 TGGCGCGCAGCAGCTTCAGCCAAACCTCCATCGCGCTCGGCGTATTGACGGCGGTAA 400  
Db 332 TCCCGCTCGACAAACAAACAAACAAAGTCTTAGCGCGCGCGCCCAAGATCAACACA 381

Qy 401 GCTATGCGCTTACCCCGAATGTCGATTTGGATTCGCGGTACCGGTACAACTACATCGGCA 460  
Db 382 ACAAGCTCAACGCGCTTCGCGGTTCACAAAGATGGGGGGTTTACAACAAACAGCAGCAACGCG 441

Qy 461 AAGTCAACACTGTCAAAACGTCGCTTCGCGGCACTGCTCGGCGTGGCGCTC 516  
Db 442 GCGGCACTACGCGGCAACGCGCGGACGCTGGAAGAGCTACTTCAACAAAGTCGCTC 497

RESULT 9  
CF589226  
LOCUS  
DEFINITION  
EST00F06 Subtracted cDNA library of JA/BTH-treated rice leaf Oryza sativa (japonica cultivar-group) cDNA clone JBI93, mRNA sequence.

ACCESSION  
CF589226

VERSION  
CF589226.1 GI:36355281

KEYWORDS  
EST.

SOURCE  
Oryza sativa (japonica cultivar-group)

ORGANISM  
Oryza sativa (japonica cultivar-group)

REFERENCE  
Yang, Y.

AUTHORS  
Subtracted cDNA library of JA/BTH-treated rice leaf

TITLE  
Unpublished (2003)

JOURNAL  
Contact: Yinong Yang

COMMENT  
Plant Pathology Department

University of Arkansas

217 Plant Sci Bldg, Fayetteville, AR 72701, USA

Tel: 501-575-5635

Fax: 501 575 7601

Email: yiyang@uark.edu

Seq primer: 17.

FEATURES  
Location/Qualifiers

1..741

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Drew (a major cultivated variety in Arkansas)"

/db\_xref="taxon:39947"

/clone="JBI93"

/tissue\_type="Seedling leaves"

/dev\_stage="16-day-old rice seedling treated by JA/BTH"

/clone\_lib="Subtracted cDNA library of JA/BTH-treated rice

leaf"

/note="Vector: pGEM-T easy; Rice seedling leaves were pretreated with 0.3 mM cycloheximide (CHX) half an hour before treatment of 0.2 mM jasmonic acid (JA) or 0.4 mM benzoethiadiazole (BTH). Both JA- and BTH-induced mRNAs were equally pooled for subtracted cDNA library construction"

# ORIGIN

Query Match 10.2%; Score 53.6; DB 6; Length 741;  
Best Local Similarity 44.5%; Pred. No. 0.00079;  
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCGACTGGCGAAGCGCATCGCGCTTTTACGTCCAAAGCGATCGCGCACAG 100  
Db 59 CAGCAGCGCGCATGGAGGGATACGACCGCGAGTTCTACCAAGTTTCAGCGACAGCTGCGGC 118

Qy 101 CAAAAGCCTCAAGCTCTTTAGTCTTGCCAAAGGCTTCAGCGCGGCATCTCCCGCAGGCT 160  
Db 119 TGCAGACGGCGAGCTTCTCGGCGCTCTCCCTCGGCGACTCCATCTGGTCTCTCCGCTCG 178

Qy 161 ACCGATCAACGACCTCCGCTTCGCGCTGCGATTAACGCGCTACAAAACTATAAAGCCC 220  
Db 179 ACCGCGCAACGAGCGCGCTTCGACGCGGAGTACCACTTCTCTCCGCTCCGCG 238

Qy 221 CATCCACGATTTCAAACTTTACAGCATCGGCGGCTCCGCGATTTACAGCTTCGACACCC 280  
Db 239 CCAAGAACGCCATCGCCAAACATCAACGCGCTCGCGGAACTCGATGGCGCGGCGCTCA 298

Qy 281 AATCGCGCGTCAAAACGATGTCGCGCGCGCTTGAGCCTCAACGCGCGCTCCGCTCGACT 340  
Db 299 TCGGCTCGGCAAGCTCGCTTCGCGCGCACCAAGCGCGACCGCTTACAACAGCGCTCAACC 358

Qy 341 TGGCGCGCAGCAGCTTCAGCCAAACCTCCATCGCGCTCGGCGTATTGACGGCGGTAA 400  
Db 359 TCCCGCTCGACAAACAAACAAACAAAGTCTTAGCGGCGCGCCCAAGATCAACACA 418

Qy 401 GCTATGCGCTTACCCCGAATGTCGATTTGGATTCGCGGTACCGGTACAACTACATCGGCA 460  
Db 419 ACAAGCTCAACGCGCTTCGCGGTTCACCAAGATGGGGGGTTTACAACAAACAGCAGCAACGCG 478

Qy 461 AAGTCAACACTGTCAAAACGTCGCTTCGCGGCACTGCTCGGCGTGGCGCTC 516  
Db 479 GCGGCACTACGCGGCAACGCGCGGACGCTGGAAGAGCTACTTCAACAAAGTCGCTC 534

# RESULT 10

CF671800

LOCUS

DEFINITION

OSJNB05117.f OSJNB Oryza sativa (japonica cultivar-group) cDNA

clone OSJNB05117 5', mRNA sequence.

ACCESSION

CF671800

VERSION

CF671800.1 GI:29675525

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartodeae; Oryzaceae; Oryza.

1 (bases 1 to 759)

Jantaseuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,

Stahlberg,B., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,

Soderlund,C. and Wang,G.L.

Large-scale identification of expressed sequence tags involved in

rice and rice blast fungus interaction

Plant Physiol. 138 (1), 105-115 (2005)

15888683

COMMENT

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 488A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288



```

Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: I column: 17
Seq primer: gta aac cga cgg cca gtc.

FEATURES
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            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nipponbare"
            /db_xref="taxon:39947"
            /clone="OSJNE05117"
            /tissue_type="Leaf"
            /dev_stage="3 week"
            /lab_host="DH10B"
            /clone_lib="OSJNE"
            /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
            XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN
    Query Match      10.2%; Score 53.6; DB 6; Length 759;
    Best Local Similarity 44.5%; Pred. No. 0.00079;
    Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 41 CGGCCGCGCACTGCGGAAGCGCATCGGCTTTTACGTCCAAAGCGGATCGGCACACG 100
DB 35 CAGCAGCGCCATGAGGAGATACGACCGCGAGTTCTACCACTTACGCGACGAGTGGCGC 94
QY 101 CAAAGCCTCAAGCTCTTTAGGTTCTGCCAAGGTTTACGCGCGCATCTCCGAGGCT 160
DB 95 TGCAGACGGCGAGCTTCTCCGCGCTCTCCCTCGCGGACTTCCATCTGGTCTCCCTCCG 154
QY 161 ACCGCATCAACGACCTCGCTTCGCGCTGATTTACACGCGCTTACAAAATATAAGGCC 220
DB 155 ACCGCGCAACGAGCGGCTTTCGAGCGGAGTACACACTTCTCTCCCTCCCTCCG 214
QY 221 CATCCACCGATTTCAAACTTTACAGCATGCGCGCTTCGCCCAATTTACGACTTCGACACC 280
DB 215 CCAAGACGCCATCGCCAACTCAACGCGCTCGCGGAACTCTGATGGCGCGGCTCA 274
QY 281 AATCGCGCTCAACCGTATCTCGGCGCGGCTTGAGCTCAACCGCGCTCCGCTGACT 340
DB 275 TCGGCTCGGCAAGCTCGCTTTCGCGCGCCACCAAGCGCGACGCTTACAAACGAGCTCAACC 334
QY 341 TGGGCGGAGCAGACAGCTTTCAGCAAACTTCCATCGCGCTGGCGTATTGACGGCGTAA 400
DB 335 TCCCGTCAACAAACAAACAAACAAAGTCTACGCGCGCGCGCCGCCAAGATCAACA 394
QY 401 GCTATGCGGTTACCCCGAATGTGATTTGGATGCGCGCTACGCTTACAACTACATCGGCA 460
DB 395 ACAAGTCAACGCTTCGGGTTCAACAGATGGGGGTTACAAACAGCAGCAACGGCG 454
QY 461 AAGTCAACACTGTCAAAAAGTTCGGTTCGGGGAAGTCTCGCGCGGCTCGCGCTC 516
DB 455 GCGGCAACTACGCGGCAACGCGCGGAGCTGTAAGAGCTACTTCAACAAAGTGGTTC 510

RESULT 11
CB677339
LOCUS
DEFINITION
    OSJNE14C19.f OSJNE Oryza sativa (japonica cultivar-group) cDNA
    clone OSJNE14C19 5', mRNA sequence.
ACCESSION
    CB677339
VERSION
    CB677339.1 GI:29681064
KEYWORDS
    EST.
ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 762)
    Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,

Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
1588683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: C column: 19
Seq primer: gta aac cga cgg cca gtc.

FEATURES
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            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
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            /clone="OSJNE14C19"
            /tissue_type="Leaf"
            /dev_stage="3 week"
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            /clone_lib="OSJNE"
            /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
            XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN
    Query Match      10.2%; Score 53.6; DB 6; Length 762;
    Best Local Similarity 44.5%; Pred. No. 0.00079;
    Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 41 CGGCCGCGCACTGCGGAAGCGCATCGGCTTTTACGTCCAAAGCGGATCGGCACACG 100
DB 33 CAGCAGCGCCATGAGGAGATACGACCGCGAGTTCTACCACTTACGCGACGAGTGGCGC 92
QY 101 CAAAGCCTCAAGCTCTTTAGGTTCTGCCAAGGTTTACGCGCGGATCTCCGAGGCT 160
DB 93 TGCAGACGGCGAGCTTCTCCGCGCTCTCCCTCGCGGACTTCCATCTGGTCTCTCCCTCCG 152
QY 161 ACCGCATCAACGACCTCGCTTCGCGCTGATTTACACGCGCTTACAAAATATAAGGCC 220
DB 153 ACCGCGCAACGAGCGCGCTTTCAGCGCGGAGTACCACTTCTCTCCCTCCCTCCG 212
QY 221 CATCCACCGATTTCAAACTTTACAGCATGCGCGGCTTCGCCAATTTACGACTTCGACACC 280
DB 213 CCAAGACGCCATCGCCAACTCAACGCGCTCGCGGAACTCTGATGGCGCGGCTCA 272
QY 281 AATCGCGCTCAACCGTATCTCGGCGCGGCTTGAGCTCAACCGCGCTCCGCTGACT 340
DB 273 TCGGCTCGGCAAGCTCGCTTTCGCGCGCCACCAAGCGCGAGCTTACAAACGAGCTCAACC 332
QY 341 TGGGCGGAGCAGACAGCTTTCAGCAAACTTCCATCGCGCTGGCGTATTGACGGCGTAA 400
DB 333 TCCCGTCAACAAACAAACAAACAAAGTCTTACGCGCGCGCGCCCAAGATCAACA 392
QY 401 GCTATGCGGTTACCCCGAATGTGATTTGGATGCGCGCTACGCTTACAACTACATCGGCA 460
DB 393 ACAAGTCAACGCTTTCGGGTTCAACAGATGGGGGTTTACAAACAGCAGCAACGGCG 452
QY 461 AAGTCAACACTGTCAAAAAGTTCGGTTCGGGGAAGTCTCGCTCGCGCTCGCGCTC 516
DB 453 GCGGCAACTACGCGGCAACGCGCGGAGCTGTAAGAGCTACTTCAACAAAGTGGTTC 508

RESULT 12
CB677062

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LOCUS      CB677062              775 bp      mRNA      linear      EST 09-APR-2003
DEFINITION OSJNEb13K18.f OSJNEc Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEb13K18 5', mRNA sequence.
ACCESSION  CB677062
VERSION     CB677062.1  GI:29680787
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 775)
AUTHORS     Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE       Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL     Plant Physiol. 138 (1), 105-115 (2005)
PUBMED      15888683
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR Primers
            FORWARD: gta aaa cga cgg cca gtc
            BACKWARD: gga aac agc tat gac cat g
            Plate: 13 row: K column: 18
            Seq primer: gta aaa cga cgg cca gtc.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39947"
                     /clone="OSJNEb13K18"
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                     /lab_host="DH10B"
                     /clone_lib="OSJNEc"
                     /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN
Query Match      10.2%; Score 53.6; DB 6; Length 775;
Best Local Similarity 44.5%; Pred. No. 0.0008;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCACTGGCGGAAGGCGATCCGGCTTTAGTCCAAAGCGCTTCAGCGCGCATCTCCGCAAGCT 100
Db 36 CAGCAGCGCGCATGGAGGGATACGACCGCGAGTCTTACAGTTCCAGCGACCAAGCTGCGGC 95

Qy 101 CAAAGCCTCAAGCTCTTTAGTCTCTGCGGCGCTTCAGCGCGCATCTCCGCAAGCTTCGCGAGCT 160
Db 96 TGCAGACGGCGAGCTTCTCCGGCTCTCTCCGCGGACTTCCATCTGGTCTCTCCCTCCGCTCG 155

Qy 161 ACCGCATCAAGACCTCGCTTGGCGGTCGATGATACCGCGCTTACAAAGCTTATTAAGGCC 220
Db 156 ACCGCGCAACGAGCGCGCTTCGACGCGAGTACCACTTCTCTCTCCCTCCCTCCCGCG 215

Qy 221 CATCCACGATTTCAAATTTACAGCATCGGGGCTCGCCATTTACGATTCGACACCC 280
Db 216 CAAAGACGCATCGCCCAACTCAACGGCGTTCGCGGAAACCTGATGGCCCGGCGCTCA 275

Qy 281 AATCGCCCGTCAAAACCGTATCTCGGCGCGCTTCGAGCTCAACCGCGCTTCAAAAGCTTCCGCT 340
Db 276 TGGGTCGCGCAAGCTTCGCTTCGGGCGCAACGAGCGCGATGATCAACAGCGTCAACC 335

Qy 341 TGGGCGGAGGACAGCTTTACAGCCAAACCTTCATCGGCTCGGCGTATTTGAGGGCGTAA 400

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Db 336 TCCCCTCGACACACACACACAAAGTCTTACGGGGGGCGCCAGATCAACACACA 395
Qy 401 GCTATGCGGTTACCCCGAATGTTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCA 460
Db 396 ACAAGCTCAACGCTTCGGGTTCAACAAGATGGGGGTTACAACAACAGCAGCAACGCG 455
Qy 461 AAGTCAACACTGTCAAAAAGTTCGCTTCGCGGCAACTGTTCGTCGGGCTGGCGGCTC 516
Db 456 GCGGCAACTACGCGGCGCAACGCGGCGACGCTGAAGAGTACTTCAACAAGTTCGGTC 511

RESULT 13
CB654692              778 bp      mRNA      linear      EST 09-APR-2003
LOCUS      OSJNEc07G20.f OSJNEc Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEc07G20 5', mRNA sequence.
ACCESSION  CB654692
VERSION     CB654692.1  GI:29658417
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 778)
AUTHORS     Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE       Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL     Plant Physiol. 138 (1), 105-115 (2005)
PUBMED      15888683
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR Primers
            FORWARD: gta aaa cga cgg cca gtc
            BACKWARD: gga aac agc tat gac cat g
            Plate: 07 row: G column: 20
            Seq primer: gta aaa cga cgg cca gtc.

FEATURES             Location/Qualifiers
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                     /clone="OSJNEc07G20"
                     /tissue_type="Leaf"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="OSJNEc"
                     /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match      10.2%; Score 53.6; DB 6; Length 778;
Best Local Similarity 44.5%; Pred. No. 0.0008;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGCACTGGCGGAAGGCGCATCCGGCTTTAGTCCAAAGCGCTTCAGCGCGCATCGCACAG 100
Db 48 CAGCAGCGCGCATGGAGGGATACGACCGCGAGTCTTACAGTTCCAGCGACCAAGCTGCGGC 107

Qy 101 CAAAGCCTCAAGCTCTTTAGTCTCTGCGGAGCTTCGCGGAGCTTCAGCGCGCATCTCCGAGGCT 160
Db 108 TGCAGACGGCGAGCTTCTCCGGCTCTCTCCGCGGACTCCATCTGGTCTCTCCCTCCGCTCG 167

Qy 161 ACCGCATCAAGACCTCGGCTTCGCGCTTCGATTTACAGCGCTTACAAAGCTTATTAAGGCC 220

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[illegible]

RESULT 14					
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LOCUS	CB665147	782 bp	mRNA	linear	EST 09-APR-2003
DEFINITION	OSJNed1lF07.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA clone OSJNed1lF07 5', mRNA sequence.				

<b>ESI.</b>	Oryza sativa (japonica cultivar-group)
<b>SOURCE</b>	Oryza sativa (japonica cultivar-group)
<b>ORGANISM</b>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.
<b>REFERENCE</b>	1 (bases 1 to 782)
<b>AUTHORS</b>	Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G., Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A., Soderlund,C. and Wang,G.L.
<b>TITLE</b>	Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction
<b>JOURNAL</b>	Plant Physiol. 138 (1), 105-115 (2005)
<b>PUBLISHED</b>	15889683

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FEATURES
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/clone="OSJNEd11P07"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEd"
/note="Vector: pluscript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"
ORIGIN

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## ORIGIN

## FEATURES

Query Match	10.2%;	Score 53.6;	DB 6;	Length 782;	
Best Local Similarity	44.5%;	Pred. No. 0.0008;			
Matches 212;	Conservative	0;	Mismatches 264;	Indels	0; Gaps 0;

  

QY	41	CGGCGCGCACATGGCGGGAAGGCGCATCGCGCTTTTACGTCGCAAGCGCATGCGCGCACACG	100
DB	38	CAGCAGGGCCATGGAGGSGATACGACCGGAGTTCTTACCAAGTTTCAGGACCACTGCGGC	97
QY	101	CAAAAGCCTCAGCTCTTTAGTTCTTGCCAAAGGCTTCAGCCCGCGCATCTCCGAGGCT	160
DB	98	TGCAGACGGCGAGCTTCTTCGCGCTCTCCCTCGCGCACTCCATCTGGTCCTCCCTCCG	157
QY	161	ACGCGCATCAAGCACTCCGCTTCGCGCGTGATTCACGCGGCTACAAAAAATATAAAGCCC	220
DB	158	ACGCGCGCAACGAGCGGCGCTTCGACGGCGAGTACCACCACCTTCTCTCCCTCCCTCCCG	217
QY	221	CATCCAACGATTTCAAACCTTTACAGCATCGGCGCGTTCGGCATTTACGATTCGACACCC	280
DB	218	CCAAGAACCGCATCGCCAAACATCAACGGGCTGCCCGGAAACCTGAGTGGCCCGGCGCTCA	277
QY	281	AATCGCCCGTCAAAACGTTATCTCGGCGCGCGCTTGAGCGCTCAACCGCGCTCCGTCGACT	340
DB	278	TGGGCTTCGGCAAGCTTCGCGTTCGGCGCCACCAAGCGCGACCGCTACACAGCGTCAACC	337
QY	341	TGGCGCGCACGACAGCTTTCAGCCAAACCTCCATCGCGCTTCGCGTATTGACGGGCGTAA	400
DB	338	TCCCGCTCGACACAAACAAACAAAGTCTTACCGCGCGCGCGCAAGATCAACAACA	397
QY	401	GCATGCGGTTACCCCGAATGTGATTCGATCCCGGCTACCGCTACCACTACATCGGCA	460
DB	398	ACACGCTCAAGCCTTCGGGTTCAACAAGATGGGGGTTACAACAACGACGACACGGCG	457
QY	461	AAGTCAACACTGTCAAAAACGTCGTTCCGGCGAACTGTCGTCGGCGTGC CGCTC	516
DB	458	GCGGCAACTACGCGGCAACGCGGCGACGTGAAGAGCTACTTCAACAAGTCGCTC	513

  

RESULT 15					
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LOCUS	OSJNED15K14.f		OSJNED15K14.f		OSJNED15K14.f
DEFINITION	clone OSJNED15K14 5', mRNA sequence.				

Accession	LOCUS	DEFINITION	842 bp	linear	EST 09-APR-2003
CB668023	LOCUS	OSJNed15K14.f OSJNed15K14.f (japonica cultivar-group) CDNA clone OSJNed15K14 5', mRNA sequence.	842 bp	linear	EST 09-APR-2003

REPORT SOURCE ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
Oryza sativa (japonica cultivar-group)	1 (bases 1 to 842)	Jantanasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.H.	Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction	Plant Physiol. 138 (1), 105-115 (2005)
Oryza sativa (japonica cultivar-group)				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiaceae; Oryzaceae; Oryza.				

University Of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: gta aaa cga cgg cca gtg  
BACKWARD: gga aac agc tat gac cat g  
Plate: 15 row: K column: 14  
Seq primer: gta aaa cga cgg cca gtg.  
Location/Qualifiers  
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source

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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/notes="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"
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## ORIGIN

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Query Match      10.2%; Score 53.6; DB 6; Length 842;
Best Local Similarity 44.5%; Pred. No. 0.0008;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy 41 CGGCGCGGCACTGGCGGAGGGCGCATCCGGCTTTTACGTCCAAAGCGGATGCCGCGACAG 100
Db 42 CAGCAGCGGCGCATGGAGGGATACGACCGCGAGTTCTACCAAGTTTCAGCGCACAGCTGCGGC 101
Qy 101 CAAAAGCCTCAAGCTCTTTAGGTTTCGCCAAGGCTTCAGCCCGGCATCTCCGCGAGCT 160
Db 102 TGCAGAGCGGAGCTTCTCCGGCTCTCCCTCGCGGACTCCATCTGTCTCTCCCTCCG 161
Qy 161 ACCGCATCAACGACCTCCGCTTCGCGCTCGATTACACGCGCTACAAAACTATAAAGCCC 220
Db 162 ACCGCGCAACGAGCGGCGCTTCGACGGCGAGTACCACCACTTCTCTCCCTCCCG 221
Qy 221 CATCCACCGATTTCAAACTTTACAGCATTCGGGGGTCGCGCATTTAGCACTTCGACACCC 280
Db 222 CCAAGAACGCGCATCGCCCAACATCAACGCGCTCGCGGAAACCTGGATGGCCGCGGCTCA 281
Qy 281 AATCGCCGTCACACCGTATCTCGCGCGGCTTGAGCCTCAACCGCGCTCCGTGCACT 340
Db 282 TCGGCTCCGCAAGCTCGCCTTCGGGCGCCACCAAGGCGGACCGCTAACAGCGTCAACC 341
Qy 341 TGGCGGCGCAGCGACAGCTTCAGGCAAACTCCATCGGCTTCGGCTATTGACGGGGTAA 400
Db 342 TCCCGTTCGACAAACAAACAAACAAAGTCTCTACGGGGGCGCGCAAGATCAACAACA 401
Qy 401 GCTATGCCGTTACCCCGAATGTGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA 460
Db 402 ACAACGTCAACGCTTCGGGTTCAACAAGATGGGGGTTACAACAACAGCAGCAACGGCG 461
Qy 461 AAGTCAACACTGTCAAAAAGCTCGTTCCGCGCACTGTCCGTCCGGGTGGGGTC 516
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 11, 2006, 15:21:38 ; Search time 115 Seconds  
(without alignments)  
632.194 Million cell updates/sec

Title: US-10-650-123-2  
Perfect score: 868  
Sequence: 1 MKKALATLIALPAALAE.....VNTKVRSGELSGVGRVKF 174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	868	100.0	174	4	US-10-428-817A-32
5	868	100.0	174	5	US-10-937-758A-36
6	864	99.5	174	4	US-10-320-800-4
7	864	99.5	174	5	US-10-988-943-20
8	825	95.0	174	4	US-10-467-534-90
9	206	23.7	241	5	US-10-988-943-16
10	122.5	14.1	94	5	US-10-795-159-735
11	103.5	11.9	350	5	US-10-946-647-1377
12	103	11.9	228	4	US-10-282-122A-69437
13	101	11.6	21	4	US-10-082-014-124
14	101	11.6	21	4	US-10-372-076-125
15	101	11.6	21	4	US-10-732-862A-139
16	101	11.6	21	4	US-10-677-074-125
17	99.5	11.5	350	4	US-10-282-122A-77105
18	99	11.4	210	4	US-10-282-122A-55523
19	98.5	11.3	350	5	US-10-946-647-1389
20	98.5	11.3	350	5	US-10-946-647-1395
21	98.5	11.3	350	5	US-10-946-647-1404
22	97	11.2	21	4	US-10-082-014-123
23	97	11.2	21	4	US-10-372-076-124
24	97	11.2	21	4	US-10-732-862A-138
25	97	11.2	21	4	US-10-677-074-124
26	97	11.2	353	4	US-10-467-421-21
27	94.5	10.9	212	3	US-09-815-242-10149

28	94.5	10.9	212	4	US-10-282-122A-42990	Sequence 42990, A
29	94	10.8	352	4	US-10-336-840-37	Sequence 37, Appli
30	94	10.8	353	4	US-10-203-942-9	Sequence 9, Appli
31	93.5	10.8	227	4	US-10-282-122A-68048	Sequence 68048, A
32	91.5	10.5	211	4	US-10-282-122A-77886	Sequence 77886, A
33	91.5	10.5	217	4	US-10-767-701-36755	Sequence 36755, A
34	90.5	10.4	443	4	US-10-282-122A-67174	Sequence 67174, A
35	89.5	10.3	257	3	US-09-815-242-13845	Sequence 13845, A
36	89	10.3	189	4	US-10-425-114-54157	Sequence 54157, A
37	89	10.3	231	4	US-10-425-114-71651	Sequence 71651, A
38	89	10.3	607	4	US-10-425-115-269306	Sequence 269306,
39	88.5	10.2	180	4	US-10-369-299-7	Sequence 7, Appli
40	88.5	10.2	346	4	US-10-467-421-90	Sequence 90, Appli
41	88.5	10.2	346	5	US-10-946-647-1413	Sequence 97, Appli
42	88.5	10.2	346	5	US-10-946-647-1413	Sequence 1413, Ap
43	88.5	10.2	346	5	US-10-946-647-1448	Sequence 1448, Ap
44	88.5	10.2	573	3	US-09-952-267-3	Sequence 3, Appli
45	88.5	10.2	573	5	US-10-872-768-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-870-759-36  
; Sequence 36, Application US/09870759  
; Patent No. US20020177551A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-870-759-36

Query Match	100.0%	Score 868;	DB 3;	Length 174;
Best Local Similarity	100.0%	Pred. No. 4.1e-85;		
Matches 174;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR	60	
Db	1	MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR	60	
Qy	61	FAVDYTRYKNYKAPSTDPLKYSIGASALYDFDTQSPVKPYLCARLSLRASVDLGGSDSF	120	
Db	61	FAVDYTRYKNYKAPSTDPLKYSIGASALYDFDTQSPVKPYLCARLSLRASVDLGGSDSF	120	
Qy	121	SQTSIGLGLVAGSVAVTFPNVDLDAGYRNYIGKVTYKVRSGELSGVGRVKF	174	
Db	121	SQTSIGLGLVAGSVAVTFPNVDLDAGYRNYIGKVTYKVRSGELSGVGRVKF	174	

RESULT 2  
US-09-751-708A-36  
; Sequence 36, Application US/09751708A  
; Publication No. US20030157113A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 751708  
; CURRENT APPLICATION NUMBER: US/09/751,708A  
; PRIOR FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/173,371  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 166

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-751-708A-36

Query Match          100.0%; Score 868; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 3
US-10-650-123-2
; Sequence 2, Application US/10650123
; Publication No. US20040132652A1
; GENERAL INFORMATION:
; APPLICANT: Shire BioChem Inc.
; TITLE OF INVENTION: PHARMACEUTICAL LIPOSOMAL COMPOSITIONS CONTAINING N.MENINGITIDIS D
; FILE REFERENCE: 74872-94
; CURRENT APPLICATION NUMBER: US/10/650,123
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,980
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: N. meningitidis strain 608B
US-10-650-123-2

Query Match          100.0%; Score 868; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 4
US-10-428-817A-32
; Sequence 32, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
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; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-428-817A-32

Query Match          100.0%; Score 868; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 5
US-10-937-758A-36
; Sequence 36, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-937-758A-36

Query Match          100.0%; Score 868; DB 5; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.1e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNRSVDLGGSDSF 120

Qy 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 SQTSGIGLVLTGVSVAVTPNVDLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
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RESULT 6  
US-10-320-800-4  
; Sequence 4, Application US/10320800  
; Publication No. US20030215469A1  
; GENERAL INFORMATION:  
; APPLICANT: ROBINSON, ANDREW  
; APPLICANT: GORRINGE, ANDREW  
; APPLICANT: HUDSON, MICHAEL  
; APPLICANT: REDDIN, KAREN  
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE  
; FILE REFERENCE: 1581.0790001  
; CURRENT APPLICATION NUMBER: US/10/320,800  
; CURRENT FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: PCT/GB99/03626  
; PRIOR FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-10-320-800-4  
Query Match 99.5%; Score 864; DB 4; Length 174;  
Best Local Similarity 99.4%; Pred. No. 1.1e-84;  
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120  
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120  
QY 121 SQTSLGLGLTGVSVAVTPNVLDLAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174  
DB 121 SQTSLGLGLTGVSVAVTPNVLDLAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174  
RESULT 7  
US-10-988-943-20  
; Sequence 20, Application US/10988943  
; Publication No. US20050176085A1  
; GENERAL INFORMATION:  
; APPLICANT: Center for Genetic Engineering and Biotechnology  
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE  
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN  
; FILE REFERENCE: Proteomics CU2003-269  
; CURRENT APPLICATION NUMBER: US/10/988,943  
; CURRENT FILING DATE: 2004-11-15  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis (group B)  
US-10-988-943-20  
Query Match 99.5%; Score 864; DB 5; Length 174;  
Best Local Similarity 99.4%; Pred. No. 1.1e-84;  
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120  
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120

QY 121 SQTSLGLGLTGVSVAVTPNVLDLAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174  
DB 121 SQTSLGLGLTGVSVAVTPNVLDLAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174  
RESULT 8  
US-10-467-534-90  
; Sequence 90, Application US/10467534  
; Publication No. US20040131625A1  
; GENERAL INFORMATION:  
; APPLICANT: Berthet, Francois-Xavier Jacques  
; APPLICANT: Lobet, Yves  
; APPLICANT: Poolman, Jan  
; APPLICANT: Verlant, Vincent Georges Christian Louis  
; TITLE OF INVENTION: Vaccine Composition  
; FILE REFERENCE: B45261  
; CURRENT APPLICATION NUMBER: US/10/467,534  
; CURRENT FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: PCT/EP02/01356  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: GB 0103169.9  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 90  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-534-90  
Query Match 95.0%; Score 825; DB 4; Length 174;  
Best Local Similarity 94.3%; Pred. No. 1.8e-80;  
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120  
DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRSYDLGSDSF 120  
QY 121 SQTSLGLGLTGVSVAVTPNVLDLAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174  
DB 121 SKTSAGLVLAGSVAVTPNVLDLAGYRNYIGKVTNKVNRSGELSVGVVRVKF 174  
RESULT 9  
US-10-988-943-16  
; Sequence 16, Application US/10988943  
; Publication No. US20050176085A1  
; GENERAL INFORMATION:  
; APPLICANT: Center for Genetic Engineering and Biotechnology  
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE  
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN  
; FILE REFERENCE: Proteomics CU2003-269  
; CURRENT APPLICATION NUMBER: US/10/988,943  
; CURRENT FILING DATE: 2004-11-15  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 241  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis (group B)  
US-10-988-943-16  
Query Match 23.7%; Score 206; DB 5; Length 241;  
Best Local Similarity 26.4%; Pred. No. 1.4e-13;  
Matches 62; Conservative 30; Mismatches 59; Indels 84; Gaps 7;  
QY 23 SGFYVQADAAHA-----KASSLSG-----AKGFSRISAGYRINDLRPA 62

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Db      8 SPYTVQADLAYAABERITHDYPKATCANNTSTVSDYFRNIRAHSHIPRVSVGYDFGWRRIA 67
Qy      63 VDYTRYKNY-----KAPSTDPKLXISIGASAIYDF--- 91
Db      68 ADYASYRKNNKNSVNTKELQKNNSGIWQELKTENQENGTFHAASSLSLSAIYDFKLN 127
Qy      92 DTQSPVKPYLGLARLSINRA-----SVDLGGSDSFSQ----- 122
Db      128 DKPDKFKYIGARVAYGHVKHQVHSVRKEITTTTSPPAQGATVPCKIVQGTNKPAYHES 187
Qy      123 ---TSIGLGVLTGVSAYVTPNDLDAGVRYNYIGKNTVKNVRSGELSVGVVRVKF 174
Db      188 NSISSLSGLGIAGVGFDITPKLTLDTGRYVHNGRLENT-RKTHEVSLGMRVYH 241

RESULT 10
US-10-795-159-735
; Sequence 735, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 28335/38615A
; CURRENT APPLICATION NUMBER: US/10/795,159
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 735
; LENGTH: 94
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-795-159-735

Query Match 14.1%; Score 122.5; DB 5; Length 94;
Best Local Similarity 33.3%; Pred. No. 3.8e-05;
Matches 30; Conservative 15; Mismatches 36; Indels 9; Gaps 2;

Qy      93 TQSPVKPYLGLARLSINRAVDLGG-----SDSFSQTSIGLGVLTGVSAYVTPNDLD 144
Db      6 TSGYTKDEFYTKLTFTKTNMPIGGDVKADQETSGRSIKRIGFGFIGGIDYITPNTILD 65

Qy      145 AGRYVNYIGKNTVKNVRSGELSVGVVRVKF 174
Db      66 LDYRNDWGRLENVR-FKTHEASFGVRYRF 94

RESULT 11
US-10-946-647-1377
; Sequence 1377, Application US/109466647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; PRIOR FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1377
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Salmonella enterica
US-10-946-647-1377

Query Match 11.9%; Score 103.5; DB 5; Length 350;
Best Local Similarity 24.3%; Pred. No. 0.026;
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Matches 50; Conservative 28; Mismatches 85; Indels 43; Gaps 8;
Qy      1 MKK-ALATLIALAPAAALAEAGSGFYVQADAAHAHAKASSLSGSAKGSFPRISAGYRIND- 58
Db      1 MKKTAIAIAVALA-----GFATVAQAAPKDNWTYAGAKLGSWSQYHDTGFIHNDG 49
Qy      59 -----LRFAVDYTRYRYKNYKAPSTD--FKLXISIGASAIYDFDTQ 94
Db      50 PTHENQLGAGAFGGYQNPVYVGFEMGYDMLGRMPYKGDNTNGAYKAQGVQLTAKLGYPIIT 109
Qy      95 SPVKPY--LGARL--SLNRRASVDLGGSDSFSQTSIGLGVLTGVSAYVTPNDLDAGVRY- 149
Db      110 DDLDDVYTRLGGVMWRADTKSNVPGGASTKHDDTGTGVSFVAGGIBYAITPEIATRLLEYQWT 169
Qy      150 NYIGKNTV-KNVRSGELSVGVVRVKF 174
Db      170 NNIGDANTIGTRPDNGLLSVGVSRYF 195

RESULT 12
US-10-282-122A-69437
; Sequence 69437, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69437
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-10-282-122A-69437

Query Match 11.9%; Score 103; DB 4; Length 228;
Best Local Similarity 25.8%; Pred. No. 0.016;
Matches 54; Conservative 23; Mismatches 90; Indels 42; Gaps 7;
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[illegible]

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RESULT 13
US-10-082-014-124
; Sequence 124, Application US/10082014
; Publication No. US20030185858A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
; FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-082-014-124

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Query Match      11.6%; Score 101; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 153 GKNTVKNVRSGELSVGVVK 173  
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Db 1 GKNTVKNVRSGELSVGVVK 21

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RESULT 14
US-10-372-076-125
; Sequence 125, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; TITLE OF INVENTION: CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-372-076-125

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Query Match      11.6%; Score 101; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy   153 GKQNTVKNVRSGELSVGRVK 173
      |||||
Db    1 GKQNTVKNVRSGELSVGRVK 21
      |||||

RESULT 15
US-10-732-862A-139
; Sequence 139, Application US/10732862A
; Publication No. US20040146524A1
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: Lyons, Katelynne J.
; APPLICANT: Jay, Haron J.
; TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICC-136.0 (4564-88881)
; CURRENT APPLICATION NUMBER: US/10/732,862A
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,123
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-732-862A-139

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Query Match      11.6%; Score 101; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 153 GKVTVKNVRSGLSVGVVK 173  
|||  
db 1 GKVTVKNVRSGLSVGVVK 21

Search completed: January 11, 2006, 15:29:45  
Job time : 116 secs



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 11, 2006, 15:22:23 ; Search time 29 Seconds  
(without alignments)  
56.725 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868

Sequence: 1 MKKALATLIALPAALAE.....VNTKVRSGELSGVGRVKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	6	US-10-984-376-7
2	862	99.3	174	6	US-10-984-376-8
3	852	98.2	174	6	US-10-984-376-10
4	852	98.2	174	6	US-10-984-376-11
5	849	97.8	174	6	US-10-984-376-9
6	846	97.5	174	6	US-10-984-376-12
7	825	95.0	174	7	US-11-103-957-90
8	809.5	93.3	175	6	US-10-467-657-2512
9	805	92.7	174	6	US-10-984-376-14
10	785.5	90.5	173	6	US-10-984-376-13
11	724	25.8	232	6	US-10-467-657-5652
12	218.5	25.2	229	6	US-10-467-657-6238
13	218	25.1	226	6	US-10-467-657-6038
14	214	24.7	281	6	US-10-467-657-8006
15	212	24.4	278	6	US-10-467-657-6726
16	210	24.2	265	6	US-10-467-657-1778
17	208	24.0	161	7	US-11-052-554A-86
18	207.5	23.9	186	6	US-10-467-657-7854
19	206	23.7	229	6	US-10-467-657-7386
20	204.5	23.6	229	6	US-10-467-657-1754
21	194.5	22.4	227	6	US-10-467-657-54
22	194.5	22.4	227	6	US-10-467-657-830
23	178	20.5	189	6	US-10-467-657-3184
24	94.5	10.9	212	7	US-11-052-554A-198
25	88.5	10.2	703	7	US-11-052-554A-97

## ALIGNMENTS

### RESULT 1

US-10-984-376-7  
; Sequence 7, Application US/10984376  
; Publication No. US20050244436A1  
; GENERAL INFORMATION:  
; APPLICANT: GIULIANI, Marzia Monica  
; APPLICANT: PIZZA, Mariagrazia  
; APPLICANT: RAPPUOLI, Rino  
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS  
; FILE REFERENCE: 2300-1609.20  
; CURRENT APPLICATION NUMBER: US/10/984.376  
; PRIORITY FILING DATE: 2004-11-09  
; PRIOR APPLICATION NUMBER: 09/979,263  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: PCT/IB00/00828  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: GB 9111692.3  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: GB 9919705.5  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: GB 0005730.7  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 7  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Nepa  
US-10-984-376-7

Query Match	100.0%;	Score 868;	DB 6;	Length 174;
Best Local Similarity	100.0%;	Pred. No. 5.2e-79;		
Matches 174;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR	60	
Db	1	MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR	60	
QY	61	FANDYTRYKTKASTDFKLSYIGASAIYDFTQSPVKPYLGLARLSINRASVDLGGSDSF	120	
Db	61	FANDYTRYKTKASTDFKLSYIGASAIYDFTQSPVKPYLGLARLSINRASVDLGGSDSF	120	
QY	121	SQTSIGLGLVNGSVYATPNVDLDAGYRNYIGKNTVKNVRSGELSGVGRVKF	174	
Db	121	SQTSIGLGLVNGSVYATPNVDLDAGYRNYIGKNTVKNVRSGELSGVGRVKF	174	

Sequence 25, Appl  
Sequence 20, Appl  
Sequence 17, Appl  
Sequence 18, Appl  
Sequence 1560, Ap  
Sequence 99, Appl  
Sequence 343, Appl  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 338, Appl  
Sequence 179, Appl  
Sequence 87, Appl  
Sequence 5, Appl  
Sequence 62, Appl  
Sequence 63, Appl  
Sequence 64, Appl  
Sequence 5, Appl  
Sequence 88, Appl  
Sequence 2704, Ap  
Sequence 142, App

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RESULT 2
US-10-984-376-8
; Sequence 8, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984.376
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-8

Query Match          99.3%; Score 862; DB 6; Length 174;
Best Local Similarity 99.4%; Pred. No. 2e-78;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Qy      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Db      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 3
US-10-984-376-10
; Sequence 10, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984.376
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-11

Query Match          99.3%; Score 862; DB 6; Length 174;
Best Local Similarity 99.4%; Pred. No. 2e-78;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Qy      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Db      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 4
US-10-984-376-11
; Sequence 11, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984.376
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-11

Query Match          98.2%; Score 852; DB 6; Length 174;
Best Local Similarity 98.3%; Pred. No. 2e-77;
Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Qy      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Db      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-10

Query Match          98.2%; Score 852; DB 6; Length 174;
Best Local Similarity 98.3%; Pred. No. 2e-77;
Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Qy      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Db      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174

RESULT 4
US-10-984-376-11
; Sequence 11, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984.376
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nsnpa
US-10-984-376-11

Query Match          98.2%; Score 852; DB 6; Length 174;
Best Local Similarity 98.3%; Pred. No. 2e-77;
Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db      1  MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db      61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Qy      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
Db      121 SOTSIGLGLTGVSVAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVRVKF 174
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NspA
US-10-984-376-12

Query Match          97.5%; Score 846; DB 6; Length 174;
Best Local Similarity 97.7%; Pred. No. 7.8e-77;
Matches 170; Conservative 1; Mismatches 3; Indels 0; Gaps 0

QY 1 MKKALATLIALPAALAAEGAGSGFYVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAAEGAGSGFYVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDPKLYSGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
QY 121 SQTSGIGLVLTGVSAYVTPNVDDL D GAGYRNYIGKNTVKNVRSSEL SVGVKVF 174
Db 121 SQTSGIGLVLTGVSAYVTPNVDDL D GAGYRNYIGKNTVKNVRSSEL SVGVKVF 174

RESULT 7
US-11-103-957-90
; Sequence 90, Application US/11103957
; Publication NO. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Bethet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-11-103-957-90

Query Match          95.0%; Score 825; DB 7; Length 174;
Best Local Similarity 94.3%; Pred. No. 9.2e-75;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0

QY 1 MKKALATLIALPAALAAEGAGSGFYVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAALAAEGAGSGFYVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDPKLYSGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDPKLYSGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDSF 120
QY 121 SQTSGIGLVLTGVSAYVTPNVDDL D GAGYRNYIGKNTVKNVRSSEL SVGVKVF 174
Db 121 SKTSAGIGLVLTGVSAYVTPNVDDL D GAGYRNYIGKNTVKNVRSSEL SVGVKVF 174

RESULT 8
US-10-467-657-2512

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; Sequence 2512, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2512
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2512

Query Match 93.3%; Score 809.5; DB 6; Length 175;
Best Local Similarity 93.1%; Pred. No. 3.1e-73;
Matches 163; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 119
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 120
Qy 120 PSQTSIGLGLTVGSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 121 PSKTSAGLGLTVGSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 175

RESULT 9
US-10-984-376-14
; Sequence 14, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984,376
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nepa
US-10-984-376-14

Query Match 90.5%; Score 785.5; DB 6; Length 173;
Best Local Similarity 93.1%; Pred. No. 7.3e-71;
Matches 162; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 59
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 120
Db 60 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 119
Qy 121 SQTSGIGLGLTVGSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 120 SOKSIALGLVLTAVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 173

RESULT 10
US-10-984-376-13
; Sequence 13, Application US/10984376
; Publication No. US2005024436A1
; GENERAL INFORMATION:
; APPLICANT: GIULIANI, Marzia Monica
; APPLICANT: RAPPUOLI, Rino
; TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
; FILE REFERENCE: 2300-1609.20
; CURRENT APPLICATION NUMBER: US/10/984,376
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: 09/979,263
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/IB00/00828
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: GB 9911692.3
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9919705.5
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: GB 0005730.7
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nepa
US-10-984-376-13

Query Match 90.5%; Score 785.5; DB 6; Length 173;
Best Local Similarity 93.1%; Pred. No. 7.3e-71;
Matches 162; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 59
Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 120
Db 60 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAASVDLGGSDS 119
Qy 121 SQTSGIGLGLTVGSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 174
Db 120 SOKSIALGLVLTAVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVVKF 173

RESULT 11
US-10-467-657-5652
; Sequence 5652, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 5652

LENGTH: 232

TYPE: PRP

ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5652

Query Match 25.8%; Score 224; DB 6; Length 232;

Best Local Similarity 27.5%; Pred. No. 3.1e-15;

Matches 64; Conservative 30; Mismatches 53; Indels 86; Gaps 9;

Qy 27 VOADAHA-----AKSSSLGSAKGP-----SPRISAGYRINDLRPAV 63

Db 1 VOADLAYAAERITHDPEPTGAKKDKKISTVSDYFRNIRTHSVHPRVSGYDFGWRIAA 60

Qy 64 DYTRYKNY-----KAPSTDFK-----LYSIGASAIYDFDT 93

Db 61 DYARYRWNNKSYVNIKRVKENNGSGKKLTQDLKTENQENGTFHVVSSGLSGLSAVYDFDT 120

Qy 94 QSPVKPYLGARLSLN--RASVDL-----GGSDSFS--QTS----- 124

Db 121 GSRFPYAGVRSVGHVHRSIDSTKKTVDVTAPPTSDGAPTYINAPQTONPHQSDS 180

Qy 125 ---IGLGLVLTGVSVAVTNPVDLDAGYRYNYIGKNTVKNVRSGLSVGVVRKF 174

Db 181 IRRVGLGVLAGVGPDIPTNLTLDTGYRYHNWGRLENTN-FKTHEASLGMYRF 232

## RESULT 12

US-10-467-657-6238

Sequence 6238, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON Spa

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 6238

LENGTH: 229

TYPE: PRP

ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6238

Query Match 25.2%; Score 218.5; DB 6; Length 229;

Best Local Similarity 27.8%; Pred. No. 1.1e-14;

Matches 64; Conservative 29; Mismatches 54; Indels 83; Gaps 8;

Qy 27 VOADAHAHA-----SSSLGSAK-----GFSPRISAGYRINDLRPAVD 64

Db 1 VOADLAYAAERITHDPEPTGKDKKISTVSDYFRNIRTHSVHPRVSGYDFGWRIAAD 60

Qy 65 YTRYKNY-----KAPS-----TDFKLYSIGASAIYDFDTQ 94

Db 61 YARYRWNNKSYVNTKRVKENNGEKNVTVQLKAENQENGTFHVVSSGLSGLSAVDFKLN 120

Qy 95 SPVKPYLGARLSLN--RASVDL-----GGSDSFS-----DSFSQTS 124

Db 121 DKFKPYIGARVAYGHVHRSIDSTKKTTEFLTAAGDGGAPTVYNNGSTQDAHQSDSIRR 180

Qy 125 IGLGLVLTGVSVAVTNPVDLDAGYRYNYIGKNTVKNVRSGLSVGVVRKF 174

Db 181 VGLGVLAGVGPDIPTNLTLDTAGYRYHNWGRLENTN-FKTHEASLGMYRF 229

## RESULT 13

US-10-467-657-6038

Sequence 6038, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON Spa

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 6038

LENGTH: 226

TYPE: PRP

ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6038

Query Match 25.1%; Score 218; DB 6; Length 226;

Best Local Similarity 28.1%; Pred. No. 1.2e-14;

Matches 59; Conservative 28; Mismatches 57; Indels 66; Gaps 7;

Qy 30 DAAHAKASSSLGSAKGP-----SPRISAGYRINDLRPAVDYTRYK--NYKAPSTDF 78

Db 18 DAAGANQKKISTVSDYFKNIRTHSIHPRVSGYDFGWRIAADYARYRWNNKYSVDI 77

Qy 79 K-----LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASV 112

Db 78 KELENKQNKRDALKTENQENGSHVAVSSGLSGLSAVDLTKLNDKFKPYIGARVAYGHVHRSI 137

Qy 113 DL-----GGSDSFS-----DSFSQTSIGLGLVLTGVSVAVTNPVDLD 144

Db 138 DSTKKTTEFLTAAGDGGAPTVYNNGSTQDAHQSDSIRRVLGLGVLAGVGPDIPTKLTLD 197

Qy 145 AGYRYNYIGKNTVKNVRSGLSVGVVRKF 174

Db 198 TGYRYHNWGRLENTN-FKTHEASLGMYRF 226

## RESULT 14

US-10-467-657-8006

Sequence 8006, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON Spa

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 8006

LENGTH: 281

